

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-43821

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1122 CAGTTCACCTTCACCTCC 1140
||| ||||| ||||| |||||
Db 2 CAGGACCACCTTCACCTTC 20

RESULT 704

US-10-266-090-47293
; Sequence 47293, Application US/10266090
; GENERAL INFORMATION:
; APPLICANT: GOFF, STEPHEN
; APPLICANT: BONAN, CAROLINE
; APPLICANT: COLBERT, MICHELLE
; APPLICANT: WANG, RONG-LIN
; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
; TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
; FILE REFERENCE: NADII.058C1
; CURRENT APPLICATION NUMBER: US/10/266,090
; PRIOR FILING DATE: 2002-10-03
; PRIOR FILING DATE: 2002-09-26
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 51812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47293
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-47293

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1137 CTCGAGCTCCACTATACC 1155
||||| ||||| ||||| |||||
Db 2 CTCGACCACCACTTAACC 20

RESULT 705

US-10-289-762-2388
; Sequence 2388, Application US/10289762
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2388
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-2388

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 963 CCAACGGTGAAGTCCAAG 981

Db 1 CGAACGGTAGAAATCCAAG 19
||||| ||||| ||||| |||||

RESULT 706

US-10-289-762-4651
; Sequence 4651, Application US/10289762
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4651
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-4651

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 758 GCCATGCGAGTTCTTCT 776
||||| ||||| ||||| |||||
Db 2 GCCATGCGAGTTCTTCT 20

RESULT 707

US-10-289-762-5845/c
; Sequence 5845, Application US/10289762
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5845
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-5845

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 816 AAGCCTGGAGTGCACGAAG 834
||||| ||||| ||||| |||||
Db 20 AAGCAGGAGTGCACGCAG 2

RESULT 708

US-10-289-845-14/c
; Sequence 14, Application US/10289845
; GENERAL INFORMATION:
; APPLICANT: Wood, Linda
; APPLICANT: Wagner, Susanne
; APPLICANT: Parodi, Luis
; TITLE OF INVENTION: Single Nucleotide Polymorphisms in GH-1
; FILE REFERENCE: 00791.US1
; CURRENT APPLICATION NUMBER: US/10/289,845
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 20

; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-289-845-14

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1011 ACTGAAAGAGGGGAG 1029
| | | | | | | | | | | | | | | | | | | | | |
Db 19 ATCTGAAAGAGGAGGAG 1

RESULT 709

US-10-293-338-5780/c
; Sequence 5780, Application US/10293338
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: 45282
; CURRENT APPLICATION NUMBER: US/10/293,338
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 8785
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5780
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-338-5780

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1247 CCGACCCCATCCCAACCC 1265
| | | | | | | | | | | | | | | | | | | | | |
Db 19 CCACGCCCAACCCCAACCC 1

RESULT 710

US-10-303-778-1350
; Sequence 1350, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
; FILE OF INVENTION: REGULATORY GENES AND USES THEREOF
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1350
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-1350

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1252 CCCATCCCCAACCCCTTC 1270
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CCCACCCCAATCCCTTC 19

RESULT 711

US-10-310-188-48869/c
; Sequence 48869, Application US/10310188
; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GE
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48869
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-48869

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1099 ACCCTGGGCTTCAGTCCCG 1117
| | | | | | | | | | | | | | | | | | | | | |
Db 20 ACCCTGGGCTCTCTCCCG 2

RESULT 712

US-10-310-188-59951/c
; Sequence 59951, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GE
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59951
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-59951

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1252 CCCATCCCCAACCCCTTC 1270
| | | | | | | | | | | | | | | | | | | | | |
Db 20 CCCTTCCCTACCCCTCC 2

RESULT 713

US-10-310-188-64522
; Sequence 64522, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GE
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64522
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-64522

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1252 CCCATCCCCAACCCCTTC 1270

Db 1 CCCAGCCCCAGCCCTCC 19
|||||

RESULT 714

US-10-317-277A-67
; Sequence 67, Application US/10317277A
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; TITLE OF INVENTION: Modulation of Estrogen-Responsive Finger Protein Expression
; CURRENT APPLICATION NUMBER: US/10/317,277A
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-317-277A-67

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1132 TTCACCTCCAGCTCCACCT 1150
|||||

Db 1 TTCTTCTGCAGCTCCACCT 19
|||||

RESULT 715

US-10-317-277A-142/c
; Sequence 142, Application US/10317277A
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; TITLE OF INVENTION: Modulation of Estrogen-Responsive Finger Protein Expression
; FILE REFERENCE: RTS-0473
; CURRENT APPLICATION NUMBER: US/10/317,277A
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 142
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-317-277A-142

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1132 TTCACCTCCAGCTCCACCT 1150
|||||

Db 20 TTCTTCTGCAGCTCCACCT 2
|||||

RESULT 716

US-10-349-143-7116/c
; Sequence 7116, Application US/10349143
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7116
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer 99-24210 for SEQ 3182,
US-10-349-143-7116

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 848 AGATTGAGATGTTAAGG 866
|||||

Db 19 AAATTGAGATGTTAGGG 1
|||||

RESULT 717

US-10-371-474-69
; Sequence 69, Application US/10371474
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: William Gaarde
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF MEK4 EXPRESSION
; FILE REFERENCE: RIS-0169
; CURRENT APPLICATION NUMBER: US/10/371,474
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US/09/676,436
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 69
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-371-474-69

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 907 ATTTCTTTGGTCTTTGCC 925
|||||

Db 1 ATTTGTTTCCTCTTTGCC 19
|||||

RESULT 718

US-10-380-126-75/c
; Sequence 75, Application US/10380126
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-1 EXPRESSION
; FILE REFERENCE: RTS-0175
; CURRENT APPLICATION NUMBER: US/10/380,126
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 09/657,042
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 75
; LENGTH: 20
; TYPE: DNA

US-10-483-424-42

US-10-483-424-42

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/ CURRENT LISTING DATE: 2000 02
; NUMBER OF SEQ ID NOS: 18992

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/ CURRENT LISTING DATE: 2000 02
; NUMBER OF SEQ ID NOS: 18992

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; LENGTH: 20
; TYPE: DNA
; ORGANISM: Xanthomonas campestris
US-60-183-791-11958

Query Match      0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1184 CCGCAGAGAGGTGGAC 1202
Db      ||||| ||||| ||||| |||||
2 CCGCAGATAGGTGGAAC 20

RESULT 724
US-60-183-791-14782
; Sequence 14782, Application US/60183791
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley G.
; APPLICANT: Hinkle, Gregory J.
; TITLE OF INVENTION: Xanthomonas campestris Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15804)B
; CURRENT APPLICATION NUMBER: US/60/183,791
; CURRENT FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 18992
; SEQ ID NO 14782
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Xanthomonas campestris
US-60-183-791-14782

Query Match      0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1118 TGCCGAGTCCACTTCAC 1136
Db      ||||| ||||| ||||| |||||
1 TGTCCAATCCAGCTTCAC 19

RESULT 725
US-10-310-188-60224/c
; Sequence 60224, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60224
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-60224

Query Match      0.6%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1235 CAGCCCTCGCTCC 1248
Db      ||||| ||||| ||||| |||||
15 CAGCCCTCGCTCC 2

RESULT 726
US-10-310-188-9791/c
; Sequence 9791, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
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; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9791
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-9791

Query Match      0.6%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1089 CTTCAACCCACCC 1102
Db      ||||| ||||| ||||| |||||
16 CTTCAACCCACCC 3

RESULT 727
US-09-155-885A-276/c
; Sequence 276, Application US/09155885A
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; APPLICANT: ROSSAU, RUDI
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA: US/09/155,885A
; FILING DATE: 08-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 276:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 276:
US-09-155-885A-276

Query Match      0.6%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 728 GCCAGGAGAAACAG 741
      |||||||
Db 18 GCCAGGAGAAACAG 5

RESULT 728
US-10-310-188-52565/c
; Sequence 52565, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 52565
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-52565

Query Match 0.6%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 876 CTCAGGCCACCACAG 889
      |||||||
Db 15 CTCAGGCCACCACAG 2

RESULT 729
US-10-453-792-276/c
; Sequence 276, Application US/10453792
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 276:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 276:
US-10-453-792-276

Query Match 0.6%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAG 741
      |||||||
Db 18 GCCAGGAGAAACAG 5

RESULT 730
US-10-606-879-276/c
; Sequence 276, Application US/10606879
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/606,879
; FILING DATE: 27-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 276:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 276:
US-10-606-879-276

Query Match 0.6%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 276:
US-10-453-792-276

Query Match 0.6%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAG 741
      |||||||
Db 18 GCCAGGAGAAACAG 5

RESULT 730
US-10-606-879-276/c
; Sequence 276, Application US/10606879
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/606,879
; FILING DATE: 27-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 276:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 276:
US-10-606-879-276

Query Match 0.6%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
```

```
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 728 GCCAGGAGAAACAG 741
Db 18 GCCAGGAGAAACAG 5

RESULT 731
PCT-US03-05326-389/c
; Sequence 389, Application PC/TUS0305326
; GENERAL INFORMATION:
; APPLICANT: Sina Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MYC and MYB Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in the MYC and MYB
; FILE REFERENCE: 400/079 (MBHB 02-1105-A)
; CURRENT APPLICATION NUMBER: PCT/US03/05326
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/418,655
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.2
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense
PCT-US03-05326-389

Query Match 0.8%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 975 GTCCAAGCTCTACT 988
Db 15 GTCCAAGCTCTACT 2

RESULT 732
PCT-US03-05326-568
; Sequence 568, Application PC/TUS0305326
; GENERAL INFORMATION:
; APPLICANT: Sina Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MYC and MYB Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in the MYC and MYB
; FILE REFERENCE: 400/079 (MBHB 02-1105-A)
; CURRENT APPLICATION NUMBER: PCT/US03/05326
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/418,655
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
```

```
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 568
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
PCT-US03-05326-568

Query Match 0.6%; Score 14; DB 1; Length 19;
Best Local Similarity 71.4%; Pred. No. 5e+02;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 975 GTCCAAGCTCTACT 988
Db 5 GUCCAAGCTCTACT 18

RESULT 733
PCT-US01-17936-12
; Sequence 12, Application PC/TUS0117936
; GENERAL INFORMATION:
; APPLICANT: The Brigham & Women's Hospital, Inc.
; TITLE OF INVENTION: FUSION OF JAZF1 AND JUJAZ1 GENES IN
; FILE REFERENCE: 05311-024W01
; CURRENT APPLICATION NUMBER: PCT/US01/17936
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/209,093
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for PCR
PCT-US01-17936-12

Query Match 0.6%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 932 CCTCTCTCTTCAAT 945
Db 7 CCTCTCTCTTCAAT 20

RESULT 734
PCT-US03-25389-521/c
; Sequence 521, Application PC/TUS0325389
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corporation
; APPLICANT: Ross, Stuart A
; TITLE OF INVENTION: Antisense Modulation Of Acyl-CoA Synthetase 1 Expression
; FILE REFERENCE: 01294/1/PCT
; CURRENT APPLICATION NUMBER: PCT/US03/25389
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: 60/403,591
; PRIOR FILING DATE: 2002-08-14
```

; NUMBER OF SEQ ID NOS: 3624
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 521
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human ACS-1 antisense
PCT-US03-25389-521

Query Match 0.6%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 GAAACAGAACACCG 748
DB 17 GAAACAGAACACCG 4
|||||

RESULT 735

PCT-US03-25389-653/c
; Sequence 653, Application PC/TUS0325389
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corporation
; TITLE OF INVENTION: Antisense Modulation Of Acyl-CoA Synthetase 1 Expression
; FILE REFERENCE: 01294/1/PCT
; CURRENT APPLICATION NUMBER: PCT/US03/25389
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: 60/403,591
; PRIOR FILING DATE: 2002-08-14
; NUMBER OF SEQ ID NOS: 3624
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 653
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human ACS-1 antisense
PCT-US03-25389-653

Query Match 0.6%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 GAAACAGAACACCG 748
DB 20 GAAACAGAACACCG 7
|||||

RESULT 736

PCT-US03-25389-1106/c
; Sequence 1106, Application PC/TUS0325389
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corporation
; TITLE OF INVENTION: Antisense Modulation Of Acyl-CoA Synthetase 1 Expression
; FILE REFERENCE: 01294/1/PCT
; CURRENT APPLICATION NUMBER: PCT/US03/25389
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: 60/403,591
; PRIOR FILING DATE: 2002-08-14
; NUMBER OF SEQ ID NOS: 3624
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1106
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human ACS-1 antisense
PCT-US03-25389-1106

Query Match 0.6%; Score 14; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 GAAACAGAACACCG 748
DB 18 GAAACAGAACACCG 5
|||||

RESULT 737

PCT-US03-25389-1315/c
; Sequence 1315, Application PC/TUS0325389
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corporation
; TITLE OF INVENTION: Antisense Modulation Of Acyl-CoA Synthetase 1 Expression
; FILE REFERENCE: 01294/1/PCT
; CURRENT APPLICATION NUMBER: PCT/US03/25389
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: 60/403,591
; PRIOR FILING DATE: 2002-08-14
; NUMBER OF SEQ ID NOS: 3624
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1315
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human ACS-1 antisense
PCT-US03-25389-1315

Query Match 0.6%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 GAAACAGAACACCG 748
DB 19 GAAACAGAACACCG 6
|||||

RESULT 738

US-09-874-162A-12
; Sequence 12, Application US/09874162A
; GENERAL INFORMATION:
; APPLICANT: Koontz, Jason
; TITLE OF INVENTION: FUSION OF JAZF1 AND JUAZ1 GENES IN
; FILE REFERENCE: 05311-024001
; CURRENT APPLICATION NUMBER: US/09/874,162A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,093
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for PCR
US-09-874-162A-12

Query Match 0.6%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 932 CCCTCCTCTTCATT 945
DB 7 CCCTCCTCTTCATT 20
|||||

RESULT 739

US-10-266-090-39932

```
; sequence 39932, Application US/10266090
; GENERAL INFORMATION:
; APPLICANT: GOFF, STEPHEN
; APPLICANT: BONAN, CAROLINE
; APPLICANT: COLBERT, MICHELLE
; APPLICANT: WANG, RONG-LIN
; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
; FILE REFERENCE: NADII.058C1
; CURRENT APPLICATION NUMBER: US/10/266,090
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 10/260,703
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/326,117
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 51812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39932
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-39932
```

```
Query Match 0.6%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1129 ACCTTCACCTCCAG 1142
Db 7 ACCTTCACCTCCAG 20
|||||
```

```
RESULT 740
PCT-US02-16840-2031
; Sequence 2031, Application PC/TUS0216840
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/046 (MEHB02-326)
; CURRENT APPLICATION NUMBER: PCT/US02/16840
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/294,140
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 6810
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2031
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
PCT-US02-16840-2031
```

```
Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 4.8e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 821 TGGAGTGCACGAAGTTG 837
Db 1 UGGAGUGGACGAGGUUG 17
|||||
```

```
RESULT 741
PCT-US02-16840-5019/c
; Sequence 5019, Application PC/TUS0216840
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
```

```
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Lev
; FILE REFERENCE: 400/046 (MEHB02-326)
; CURRENT APPLICATION NUMBER: PCT/US02/16840
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/294,140
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 6810
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5019
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
PCT-US02-16840-5019
```

```
Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1112 GTCCCGTGCCCGAGTTCC 1128
Db 17 GTCCACTGCCCGAGTTCC 1
|||||
```

```
RESULT 742
PCT-US02-16840A-2031
; Sequence 2031, Application PC/TUS0216840A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Lev
; FILE REFERENCE: 400/046 (MEHB02-326)
; CURRENT APPLICATION NUMBER: PCT/US02/16840A
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/294,140
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 6810
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2031
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
PCT-US02-16840A-2031
```

```
Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 4.8e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 821 TGGAGTGCACGAAGTTG 837
Db 1 UGGAGUGGACGAGGUUG 17
|||||
```

```
RESULT 743
PCT-US02-16840A-5019/c
; Sequence 5019, Application PC/TUS0216840A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Lev
; FILE REFERENCE: 400/046 (MEHB02-326)
; CURRENT APPLICATION NUMBER: PCT/US02/16840A
```

; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/294,140
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 6810
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5019
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
PCT-US02-16840A-5019

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1112 GTCCCGTCCCGAGTTCC 1128
||| |||||
Db 17 GTCCACTGCCAGTTCC 1

RESULT 744

US-09-277-026B-6346
; Sequence 6346, Application US/09277026B
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: Roberts, Elisabeth
; APPLICANT: Jarvis, Thale
; APPLICANT: Coeshott, Claire
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Method and Reagents for the Treatment of Diseases or Conditions R
; TITLE OF INVENTION: to Molecules Involved in Angiogenic Responses
; FILE REFERENCE: MBH00-824-A (239/121)
; CURRENT APPLICATION NUMBER: US/09/277,026B
; CURRENT FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/079,678
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 6652
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6346
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Oligonucleotide substrate
US-09-277-026B-6346

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 4.8e+02;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 787 GAGTGTGTCTCCTGTAG 803
||| :|||:
Db 1 GACUUGUCCUGUAG 17

RESULT 745

US-09-277-026B-6359/c
; Sequence 6359, Application US/09277026B
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: Roberts, Elisabeth
; APPLICANT: Jarvis, Thale
; APPLICANT: Coeshott, Claire
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Method and Reagents for the Treatment of Diseases or Conditions R
; TITLE OF INVENTION: to Molecules Involved in Angiogenic Responses
; FILE REFERENCE: MBH00-824-A (239/121)

; CURRENT APPLICATION NUMBER: US/09/277,026B
; CURRENT FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/079,678
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 6652
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6359
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Oligonucleotide substrate
US-09-277-026B-6359

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 863 AGGCAGCTGAGACTCA 879
||| |||||
Db 17 AGAAACTGAGGACTCA 1

RESULT 746

US-09-572-021-2010/c
; Sequence 2010, Application US/09572021
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, Jim
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McLaughlin, Fiona
; APPLICANT: Randi, Anna Maria
; TITLE OF INVENTION: Method and Reagent for the Inhibition of ERG
; FILE REFERENCE: 249/006
; CURRENT APPLICATION NUMBER: US/09/572,021
; CURRENT FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 5366
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2010
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-572-021-2010

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 752 GCACCTGCCATGACGT 768
||| |||||
Db 17 GCACATGCCATGACGT 1

RESULT 747

US-09-740-332-1266
; Sequence 1266, Application US/09740332
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Reli
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1266
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:

; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-1266

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 4.8e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1085 CAGGCTTACCCACC 1101
||||: |||||
Db 1 CAGGCUCCACCCCAUC 17

RESULT 748

US-09-780-164-840/c
; Sequence 840, Application US/09780164
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 840
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-840

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 799 TGTGTAACCTAAGAA 815
||||: |||||
Db 17 TGTGTAACCTAAGAA 1

RESULT 749

US-09-817-879-1266
; Sequence 1266, Application US/09817879
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1266
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-1266

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 4.8e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1085 CAGGCTTACCCACC 1101
||||: |||||
Db 1 CAGGCUCCACCCCAUC 17

RESULT 750

US-09-825-805-676/c
; Sequence 676, Application US/09825805
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleotides
; FILE REFERENCE: MBH00-831-F (400/009)
; CURRENT APPLICATION NUMBER: US/09/825,805
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/578,223
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 09/476,387
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1558
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 676
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-825-805-676

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1112 GTCCCGTGCCAGTTCC 1128
||||: |||||
Db 17 GTCCACTGCCAGTTCC 1

RESULT 751

US-09-827-395A-328
; Sequence 328, Application US/09827395A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MBH00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 328
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-328

Query Match 0.6%; Score 13.8; DB 1; Length 17;

Best Local Similarity 76.5%; Pred. No. 4.8e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1045 ACTAAGCCCTGGCCCC 1061
Db 1 ACUGAGGCCUGGCCCC 17

RESULT 752
US-09-848-754A-61/c
; Sequence 61, Application US/09848754A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBH00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-61

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 860 TTAAGGCCTGAGGAC 876
Db 17 TTGAGGCAATGAGGAC 1

RESULT 753
US-09-848-754A-2182/c
; Sequence 2182, Application US/09848754A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBH00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2182
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-2182

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 859 GTTAAGGCCTGAGGA 875
Db 17 GTTGAGGCAATGAGGA 1

RESULT 754
US-09-863-041A-583
; Sequence 583, Application US/09863041A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: 400/022 (MBH00-812-D)

; CURRENT APPLICATION NUMBER: US/09/863,041A
; CURRENT FILING DATE: 2001-05-22
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 583
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-863-041A-583

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 4.8e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCAACCCCC 1267
Db 1 CCCCAUCCCAUCCUCC 17

RESULT 755
US-09-864-785-583
; Sequence 583, Application US/09864785
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: 400/022 (MBH00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 583
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-583

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 4.8e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCAACCCCC 1267
Db 1 CCCCAUCCCAUCCUCC 17

RESULT 756
US-10-017-974-8720/c
; Sequence 8720, Application US/10017974
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid-Based Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBH00,1109-A (400/037)
; CURRENT APPLICATION NUMBER: US/10/017,974
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 37080
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8720
; LENGTH: 17
; TYPE: RNA
; ORGANISM: West Nile virus
US-10-017-974-8720


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Query Match
Best Local Similarity 0.6%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 995 TTTGTGGGAATCGACA 1011
Db 17 TTTCTGGGAATCAACA 1

RESULT 757
US-10-156-306-5078/c
; Sequence 5078, Application US/10156306
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5078
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-5078

Query Match
Best Local Similarity 0.6%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1204 CCCTATCAGGGGCTGA 1220
Db 17 CCATATCAGGGGCTGA 1

RESULT 758
US-10-163-552-364/c
; Sequence 364, Application US/10163552
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level
; FILE REFERENCE: MBH01-1653-A (400/014)
; CURRENT APPLICATION NUMBER: US/10/163,552
; CURRENT FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 1997
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 364
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-163-552-364

Query Match
Best Local Similarity 0.6%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1112 GTCCCGTCCCGAGTTC 1128
Db 17 GTCCACTGCCCGAGTTC 1

RESULT 759
US-10-238-700-3352
; Sequence 3352, Application US/10238700
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MBH01-1158-A)
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; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3352
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-3352

Query Match
Best Local Similarity 0.6%; Score 13.8; DB 1; Length 17;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 821 TGGAGTCGACGAAGTTG 837
Db 1 UGGAGUGGACGAGGUG 17

RESULT 760
US-10-294-037A-1194
; Sequence 1194, Application US/10294037A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli O157:H7:EDL933, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,037A
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 2772
; SOFTWARE: Proprietary
; SEQ ID NO 1194
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Escherichia coli O157:H7:EDL933, complete genome.
; FEATURE:
; LOCATION: (1711581)...(1711596)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectonObjectNumber = 1
US-10-294-037A-1194

Query Match
Best Local Similarity 0.6%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 890 TGCTGTTGCCCGCTGTC 906
Db 1 TGATGTTGCCCGCTGTC 17

RESULT 761
US-10-303-778-3691
; Sequence 3691, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3691
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-3691

Query Match
Best Local Similarity 0.6%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 1251 CCCCATCCCCAACCCCC 1267
Db 1 CCCCATCCCCCTCCCC 17

RESULT 762

US-10-310-188-5982
; Sequence 5982, Application US/10310188
; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5982
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-5982

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCAACCCCC 1267
Db 1 CCCCATCCCCCTCCCC 17

RESULT 763

US-10-310-188-7330/c
; Sequence 7330, Application US/10310188
; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7330
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-7330

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1169 CCAACTTTCGGCTCCC 1185
Db 17 CCAACTTTCGGCTCCC 1

RESULT 764

US-10-310-188-72805/c
; Sequence 72805, Application US/10310188
; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72805

; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-72805

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCAACCCCC 1267
Db 17 CCCCATCCCCACCCCC 1

RESULT 765

US-10-310-188-72831/c
; Sequence 72831, Application US/10310188
; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72831
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-72831

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCAACCCCC 1267
Db 17 CCCCATCCCCACCCCC 1

RESULT 766

US-10-316-954-1929
; Sequence 1929, Application US/10316954
; GENERAL INFORMATION:

; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli O157:H7, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/316,954
; NUMBER OF SEQ ID NOS: 5998
; SOFTWARE: Proprietary
; SEQ ID NO 1929
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Escherichia coli O157:H7, complete genome.
; FEATURE:
; LOCATION: (1627606)...(1627622)
; OTHER INFORMATION: Chromosome = 1 Strand = positive
US-10-316-954-1929

Query Match

Best Local Similarity 88.2%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 890 TGCTGTTCCTGCTGTC 906
Db 1 TGATGTTCCGCTGCTC 17

RESULT 767

US-10-430-882-328
; Sequence 328, Application US/10430882

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Lawrence Blatt
APPLICANT: James McSwiggen
APPLICANT: Bharat Chowrira
APPLICANT: Peter Haerberli
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
FILE REFERENCE: MBH800-878-H (400/112)
CURRENT APPLICATION NUMBER: US/10/430,882
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 09/827,395
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/780,533
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: PCT/US01/04273
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/181,797
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: PCT/US02/10512
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 3617
SOFTWARE: PatentIn version 3.0
SEQ ID NO 328
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-430-882-328

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 4.8e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1045 ACTAAGCCCCCTGGCCCC 1061
DB 1 ACUGAGGCCUGGCCCC 17

RESULT 768

US-10-471-271-328
Sequence 328, Application US/10471271
GENERAL INFORMATION:
APPLICANT: Blatt, Lawrence
APPLICANT: Chowrira, Bharat
APPLICANT: Haerberli, Peter
APPLICANT: McSwiggen, James
APPLICANT: Fosnaugh, Kathy
TITLE OF INVENTION: Modulation of Gene Expression Associated with Inflammation Prolif
FILE REFERENCE: MBHB 02-258-PCT (400/045)
CURRENT APPLICATION NUMBER: US/10/471,271
CURRENT FILING DATE: 2003-09-05
PRIOR APPLICATION NUMBER: 60/181,797
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 09/780,533
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 09/827,395
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/294,412
PRIOR FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: 60/315,315
PRIOR FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 13274
SOFTWARE: PatentIn version 3.0
SEQ ID NO 328
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-471-271-328

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 4.8e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1045 ACTAAGCCCCCTGGCCCC 1061
DB 1 ACUGAGGCCUGGCCCC 17

RESULT 769

US-10-471-271-1547/c
Sequence 1547, Application US/10471271
GENERAL INFORMATION:
APPLICANT: Blatt, Lawrence
APPLICANT: Chowrira, Bharat
APPLICANT: Haerberli, Peter
APPLICANT: McSwiggen, James
APPLICANT: Fosnaugh, Kathy
TITLE OF INVENTION: Modulation of Gene Expression Associated with Inflammation Pro
FILE REFERENCE: MBHB 02-258-PCT (400/045)
CURRENT APPLICATION NUMBER: US/10/471,271
CURRENT FILING DATE: 2003-09-05
PRIOR APPLICATION NUMBER: 60/181,797
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 09/780,533
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 09/827,395
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/294,412
PRIOR FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: 60/315,315
PRIOR FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 13274
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1547
LENGTH: 17
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-471-271-1547

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1204 CCTATCAGGGGGCTGA 1220
DB 17 CCTATCAGGGGGCTGA 1

RESULT 770

US-10-669-841-3859
Sequence 3859, Application US/10669841
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Lawrence, Blatt
APPLICANT: Dennis, Macejak
APPLICANT: James, McSwiggen
APPLICANT: David, Morrissey
APPLICANT: Pamela, Pavco
APPLICANT: Patricia, Lee
APPLICANT: Kenneth, Draper
APPLICANT: Elisabeth, Roberts
TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND H
FILE REFERENCE: 400/042US (MBHB02-249-E)
CURRENT APPLICATION NUMBER: US/10/669,841
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: PCT/US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/335,059
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: US 60/337,055

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/ PRIOR FILING DATE: 2001-12-05
/ PRIOR APPLICATION NUMBER: US 60/358,580
/ PRIOR FILING DATE: 2002-02-20
/ PRIOR APPLICATION NUMBER: US 60/363,124
/ PRIOR FILING DATE: 2002-03-11
/ PRIOR APPLICATION NUMBER: US 09/817,879
/ PRIOR FILING DATE: 2001-03-26
/ PRIOR APPLICATION NUMBER: US 09/740,332
/ PRIOR FILING DATE: 2000-12-18
/ PRIOR APPLICATION NUMBER: US 09/611,931
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: US 09/504,321
/ PRIOR FILING DATE: 2000-02-15
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 16207
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 3859
/ LENGTH: 17
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-3859

Query Match          0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 4.8e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1085 CAGGCTTCACCCACC 1101
DB 1 CAGGCTTCACCCACC 17

RESULT 771
US-10-707-147-5148
/ Sequence 5148, Application US/10707147
/ GENERAL INFORMATION:
/ APPLICANT: ROSETTA GENOMICS LTD
/ TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
/ FILE REFERENCE: 49992
/ CURRENT APPLICATION NUMBER: US/10/707,147
/ CURRENT FILING DATE: 2003-11-24
/ NUMBER OF SEQ ID NOS: 20189
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 5148
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-707-147-5148

Query Match          0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 752 GCACCTGCATGAGGT 768
DB 1 GCACCTGCATGAGGT 17

RESULT 772
US-10-723-361-971
/ Sequence 971, Application US/10723361
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharron G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART
/ FILE REFERENCE: PB0105
/ CURRENT APPLICATION NUMBER: US/10/723,361
/ CURRENT FILING DATE: 2003-11-26
/ PRIOR APPLICATION NUMBER: US 09/866,108
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
```

```
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART
/ FILE REFERENCE: PB0105
/ CURRENT APPLICATION NUMBER: US/10/723,361
/ CURRENT FILING DATE: 2003-11-26
/ PRIOR APPLICATION NUMBER: US 09/866,108
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Acomica Sequence Listing Engine
/ SEQ ID NO 971
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-723-361-971

Query Match          0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1053 CCGGCCCCAACCCAA 1069
DB 1 CCGGCCCCAACCCAA 17

RESULT 773
US-10-723-361-972
/ Sequence 972, Application US/10723361
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharron G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART
/ FILE REFERENCE: PB0105
/ CURRENT APPLICATION NUMBER: US/10/723,361
/ CURRENT FILING DATE: 2003-11-26
/ PRIOR APPLICATION NUMBER: US 09/866,108
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
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RESULT 774
US-10-724-270-2031
; Sequence 2031, Application US/10724270
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/046-US (MHB02-326-A)
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US/10/724,270
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/294,140
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 10/238,700
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/157,580
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aemica Sequence Listing Engine
; SEQ ID NO 972
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-724-270-361-972

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1054 CTGGCCCAACCCAG 1070
DB 1 CAGGCCCAAGCCCAAG 17

RESULT 774
US-10-724-270-2031
; Sequence 2031, Application US/10724270
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/046-US (MHB02-326-A)
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US/10/724,270
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/294,140
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 10/238,700
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/157,580
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 6810
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2031
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-724-270-2031

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 4.8e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 821 TGGAGTGCACGAGTTG 837
DB 1 UGGAGUGGACGAGGUG 17

RESULT 775
US-10-724-270-5019/c
; Sequence 5019, Application US/10724270
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/046-US (MHB02-326-A)
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US/10/724,270
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/294,140
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 10/238,700
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/157,580
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 6810
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5019
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-724-270-5019

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1112 GTCCCTGCCCCAGTTC 1128
DB 17 GTCCACTGCCAGTTC 1

RESULT 776
PCT-US03-37416-20
; Sequence 20, Application PC/TUS0337416
; GENERAL INFORMATION:
; APPLICANT: Scios, Inc.
; APPLICANT: Feng, Ying
; APPLICANT: Higgins, Linda
; APPLICANT: Kapoun, Ann
; APPLICANT: Liu, David
; APPLICANT: Schreiner, George
; TITLE OF INVENTION: METHOD FOR COUNTERACTING A PATHOLOGIC
; FILE REFERENCE: 39739-0029
; CURRENT APPLICATION NUMBER: PCT/US03/37416
; CURRENT FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: 60/504585
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/429046
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA

; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: primer
 PCT-US03-37416-20

Query Match 0.6%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 5.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1134 CACCTCAGCTCCACCT 1150
 ||||| ||||| |||||
 Db 1 CACCTTCAGCGCCACCT 17

RESULT 777

PCT-US96-00362A-67

; Sequence 67, Application PC/TUS9600362A
 ; GENERAL INFORMATION:
 ; APPLICANT: Yang, Soo Young
 ; APPLICANT: Cerab, Nezh
 ; TITLE OF INVENTION: Methods and Reagents for Typing HLA
 ; TITLE OF INVENTION: Class I Genes
 ; NUMBER OF SEQUENCES: 84
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Oppedahl & Larson
 ; STREET: 1992 Commerce Street Suite 309
 ; CITY: Yorktown
 ; STATE: NY
 ; COUNTRY: US
 ; ZIP: 10598

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
 ; COMPUTER: IBM compatible
 ; OPERATING SYSTEM: MS DOS
 ; SOFTWARE: Word Perfect

; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US96/00362A
 ; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Larson, Marina T.

; REGISTRATION NUMBER: 32, 038

; REFERENCE/DOCKET NUMBER: MSK.P-001-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (914) 245-3252

; TELEFAX: (914) 962-4330

; TELEX:

; INFORMATION FOR SEQ ID NO: 67:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; HYPOTHETICAL: no

; ANTI-SENSE: yes

; FRAGMENT TYPE: internal

; ORIGINAL SOURCE:

; ORGANISM: human

; FEATURE:

; OTHER INFORMATION: hybridization probe GE2-183 for typing of HLA Class I genes

PCT-US96-00362A-67

Query Match 0.6%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 5.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAACAGAACACC 747
 ||||| ||||| |||||
 Db 2 AGGAGACAGAACACC 18

RESULT 778

US-07-999-706-5

; Sequence 5, Application US/07999706
 ; GENERAL INFORMATION:

; APPLICANT: Denner, Larry A.
 ; APPLICANT: Rege, Ajay A.

; APPLICANT: Dixon, Richard A.F.
 ; TITLE OF INVENTION: ANTISENSE MOLECULES DIRECTED AGAINST A

; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR RECEPTOR GENE
 ; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &

; ADDRESSEE: Milnamow, Ltd.
 ; STREET: 180 North Stetson, Suite 4700

; CITY: Chicago
 ; STATE: Illinois

; COUNTRY: USA
 ; ZIP: 60601

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/999,706
 ; FILING DATE: 19921231

; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:

; NAME: Katz, Martin L.
 ; REGISTRATION NUMBER: 25,011

; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 616-5400

; TELEFAX: (312) 616-5460
 ; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 18 base pairs

; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: single

; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)

US-07-999-706-5

Query Match 0.6%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 5.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1134 CACCTCAGCTCCACCT 1150
 ||||| ||||| |||||

Db 2 CACTTCAGCTCCACAT 18

RESULT 779

US-08-170-096-5

; Sequence 5, Application US/08170096
 ; GENERAL INFORMATION:

; APPLICANT: Denner, Larry A.
 ; APPLICANT: Rege, Ajay A.

; APPLICANT: Dixon, Richard A.F.
 ; TITLE OF INVENTION: ANTISENSE MOLECULES DIRECTED AGAINST A

; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR RECEPTOR GENE FAMILY
 ; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dressler, Goldsmith, Shore &

; ADDRESSEE: Milnamow, Ltd.
 ; STREET: 180 North Stetson, Suite 4700

; CITY: Chicago
 ; STATE: Illinois

; COUNTRY: USA
 ; ZIP: 60601

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

```
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/170,096
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/999,706
; FILING DATE: December 31, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Katz, Martin L.
; REGISTRATION NUMBER: 25,011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-170-096-5

Query Match 0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1134 CACCTCCAGCTCCACCT 1150
Db 2 CACTCCAGCTCCACAT 18

RESULT 780
US-09-342-375-67
; Sequence 67, Application US/09342375
; GENERAL INFORMATION:
; APPLICANT: Yang, Soo Young
; APPLICANT: Cereb, Nezh
; TITLE OF INVENTION: Methods and Reagents for Typing HLA
; TITLE OF INVENTION: Class I Genes
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson LLP
; STREET: P.O. Box 5270
; CITY: Frisco
; STATE: CO
; COUNTRY: US
; ZIP: 80443
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/342,375
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,081
; FILING DATE: December 22, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Larson, Marina T.
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: MSK.P-001-DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (970) 668-2050
; TELEFAX: (970) 668-2082
; TELEX:
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
```

```
;
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: no
; ANTI-SENSE: yes
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; OTHER INFORMATION: hybridization probe GE2-183 for typing of HLA Class I gene:
; US-09-342-375-67

Query Match 0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAAACACC 747
Db 2 AGGAGACACGGACACC 18

RESULT 781
US-09-668-558A-94/c
; Sequence 94, Application US/09668558A
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Fruebis, Joachim
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: Methods Of Screening For Compounds That Modulate the
; TITLE OF INVENTION: LSR-Leptin Interaction and Their Use in the Prevention
; TITLE OF INVENTION: and Treatment of Obesity-Related Diseases
; FILE REFERENCE: 70.US2.REG
; CURRENT APPLICATION NUMBER: US/09/668,558A
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/155,506
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: Patent.pm
; SEQ ID NO 94
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide zinc finger nucleotides of SEQID1
; US-09-668-558A-94

Query Match 0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1235 CAGCCCTCGCTCCGAC 1251
Db 17 CAGCCCTCGCTCCGAC 1

RESULT 782
US-09-668-558B-94/c
; Sequence 94, Application US/09668558B
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Fruebis, Joachim
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: Methods Of Screening For Compounds That Modulate the
; TITLE OF INVENTION: LSR-Leptin Interaction and Their Use in the Prevention
; TITLE OF INVENTION: and Treatment of Obesity-Related Diseases
; FILE REFERENCE: 70.US2.REG
; CURRENT APPLICATION NUMBER: US/09/668,558B
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,506
; PRIOR FILING DATE: 1999-09-22
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; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: Patent.pm
; SEQ ID NO 94
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide Zinc finger nucleotides of SEQID1
US-09-668-558B-94

Query Match      0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1235 CAGCCCTCCGCTCCGAC 1251
Db 17 CAGCCCTCGCTCCAC 1

RESULT 783
US-09-703-708-14873
; Sequence 14873, Application US/09703708
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley G.
; APPLICANT: Hinkle, Gregory J.
; TITLE OF INVENTION: Xanthomonas campestris Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15904)C
; CURRENT APPLICATION NUMBER: US/09/703,708
; CURRENT FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/164,320
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/183,791
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 18992
; SEQ ID NO 14873
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Xanthomonas campestris
US-09-703-708-14873

Query Match      0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 964 CAACGGTGGAGTCCAA 980
Db 1 CAATGGTGAAGGCCAA 17

RESULT 784
US-09-969-373-4117/c
; Sequence 4117, Application US/09969373
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Haug, Brian W.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 4117
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-4117

Query Match      0.6%; Score 13.8; DB 1; Length 18;
```

```
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 912 CTTGGTCTTTGCCTTT 928
Db 18 CTTGGTTTGCCTTT 2

RESULT 785
US-10-266-090-50685/c
; Sequence 50685, Application US/10266090
; GENERAL INFORMATION:
; APPLICANT: GOFF, STEPHEN
; APPLICANT: BONAN, CAROLINE
; APPLICANT: COLBERT, MICHELLE
; APPLICANT: WANG, RONG-LIN
; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
; FILE REFERENCE: NADII.058C1
; CURRENT APPLICATION NUMBER: US/10/266,090
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 10/260,703
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/326,117
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 51812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50685
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-50685

Query Match      0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1134 CACCTCCAGTCCACCT 1150
Db 18 CACCACCACTCCACCT 2

RESULT 786
US-10-266-090-50690
; Sequence 50690, Application US/10266090
; GENERAL INFORMATION:
; APPLICANT: GOFF, STEPHEN
; APPLICANT: BONAN, CAROLINE
; APPLICANT: COLBERT, MICHELLE
; APPLICANT: WANG, RONG-LIN
; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
; FILE REFERENCE: NADII.058C1
; CURRENT APPLICATION NUMBER: US/10/266,090
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 10/260,703
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/326,117
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 51812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50690
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-50690

Query Match      0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
```


Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1134 CACCTCCAGCTCCACCT 1150
| | | | |
Db 1 CACCACCACCTCCACCT 17

RESULT 787

US-10-303-778-5025/c
; Sequence 5025, Application US/10303778

; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL

; FILE REFERENCE: 47416

; CURRENT APPLICATION NUMBER: US/10/303,778

; CURRENT FILING DATE: 2002-11-26

; NUMBER OF SEQ ID NOS: 17608

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5025

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-303-778-5025

Query Match

Best Local Similarity 0.6%; Score 13.8; DB 1; Length 18;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1250 ACCCATCCCAACCCC 1266
| | | | |
Db 18 ACCCATCCCAACCCC 2

RESULT 788

US-10-310-188-6215

; Sequence 6215, Application US/10310188

; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE

; FILE REFERENCE: 47487

; CURRENT APPLICATION NUMBER: US/10/310,188

; CURRENT FILING DATE: 2002-12-19

; NUMBER OF SEQ ID NOS: 86841

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6215

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-310-188-6215

Query Match

Best Local Similarity 0.6%; Score 13.8; DB 1; Length 18;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1237 GCCCTGCCTCCGACCC 1253
| | | | |
Db 1 GCCCTGCCTCCGACCC 17

RESULT 789

US-10-310-188-9756/c

; Sequence 9756, Application US/10310188

; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE

; FILE REFERENCE: 47487

; CURRENT APPLICATION NUMBER: US/10/310,188

; CURRENT FILING DATE: 2002-12-19

; NUMBER OF SEQ ID NOS: 86841

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9756

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-310-188-9756

Query Match

Best Local Similarity 0.6%; Score 13.8; DB 1; Length 18;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1127 CCACCTTCACCTCCAGC 1143
| | | | |
Db 17 CCACCTTCACCTCCATC 1

RESULT 790

US-10-310-188-10552/c

; Sequence 10552, Application US/10310188

; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G

; FILE REFERENCE: 47487

; CURRENT APPLICATION NUMBER: US/10/310,188

; CURRENT FILING DATE: 2002-12-19

; NUMBER OF SEQ ID NOS: 86841

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 10552

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-310-188-10552

Query Match

Best Local Similarity 0.6%; Score 13.8; DB 1; Length 18;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1250 ACCCATCCCAACCCC 1266
| | | | |
Db 18 ACCCATCCCAACCCC 2

RESULT 791

US-10-310-188-21226

; Sequence 21226, Application US/10310188

; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G

; FILE REFERENCE: 47487

; CURRENT APPLICATION NUMBER: US/10/310,188

; CURRENT FILING DATE: 2002-12-19

; NUMBER OF SEQ ID NOS: 86841

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 21226

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-310-188-21226

Query Match

Best Local Similarity 0.6%; Score 13.8; DB 1; Length 18;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 779 GAGAAACGAGTGTGTC 795
| | | | |
Db 1 GAGAAACGAGTGTGTC 17

RESULT 792

US-10-310-188-24811/c

; Sequence 24811, Application US/10310188

; GENERAL INFORMATION:

```
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24811
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-24811

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1238 CCCTCGCTCCGACCCC 1254
      |||||
Db 17 CCCTGCCCTCTACCCC 1

RESULT 793
US-10-310-188-25793
; Sequence 25793, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25793
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-25793

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1133 TCACCTCCAGTCCACC 1149
      |||||
Db 1 TCTCTCCACCTCCACC 17

RESULT 794
US-10-310-188-30755/c
; Sequence 30755, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30755
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-30755

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1006 TCGACACCTGAAAGA 1022
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Db 17 TGGACACCTGACAAAGA 1
      |||||
RESULT 795
US-10-310-188-34820/c
; Sequence 34820, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34820
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-34820

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1120 CCAGTTCACCTTCAC 1136
      |||||
Db 17 CCCAATCCCACCTTCAC 1

RESULT 796
US-10-310-188-35499
; Sequence 35499, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35499
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-35499

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1235 CAGCCCTCGCTCCGAC 1251
      |||||
Db 1 CAGCCCTCGCGCGGCC 17

RESULT 797
US-10-310-188-39123/c
; Sequence 39123, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39123
; LENGTH: 18
; TYPE: DNA
```

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; ORGANISM: Homo sapiens
US-10-310-188-39123

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCCAACCCCT 1267
    ||||| ||||| |||||
Db 18 CCCCATCCCCCTACTCTCC 2

RESULT 798
US-10-310-188-55156
; Sequence 55156, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55156
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-55156

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 753 CACCTGCGCATGCAGTT 769
    ||||| ||||| |||||
Db 1 CACCGGCTATGCAGTT 17

RESULT 799
US-10-310-188-60065/c
; Sequence 60065, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60065
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-60065

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCCAACCCCT 1267
    ||||| ||||| |||||
Db 18 CCCCATCCCCCTCCACCCCT 2

RESULT 800
US-10-310-188-72778/c
; Sequence 72778, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72778
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-72778

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCCAACCCCT 1267
    ||||| ||||| |||||
Db 18 CCCCATCCCCCTCCACCCCT 2
```

```
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72778
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-72778

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCCAACCCCT 1267
    ||||| ||||| |||||
Db 17 CCCCATCCCCCAACCCCT 1

RESULT 801
US-10-310-188-72795/c
; Sequence 72795, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72795
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-72795

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCCAACCCCT 1267
    ||||| ||||| |||||
Db 17 CCCCATCCCCCAACCCCT 1

RESULT 802
US-10-310-188-72796/c
; Sequence 72796, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72796
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-72796

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1252 CCCATCCCCCAACCCCT 1268
    ||||| ||||| |||||
Db 18 CCCATCCCCCAACCCCT 2
```

```
RESULT 803
US-10-310-188-72799/c
; Sequence 72799, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72799
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-72799

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCACCCCC 1267
Db 18 CCCACCCCCACCCCC 2

RESULT 804
US-10-310-188-85927/c
; Sequence 85927, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85927
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-85927

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 926 TTTTATCCCTCTCTTC 942
Db 18 TCTTATTCCTCTCTTC 2

RESULT 805
US-10-718-948-20
; Sequence 20, Application US/10718948
; GENERAL INFORMATION:
; APPLICANT: Feng, Ying
; APPLICANT: Higgins, Linda
; APPLICANT: Kapoun, Ann
; APPLICANT: Liu, David
; APPLICANT: Schreiner, George
; TITLE OF INVENTION: METHOD FOR COUNTERACTING A PATHOLOGIC
; FILE REFERENCE: 39739-0029
; CURRENT APPLICATION NUMBER: US/10/718,948
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/504585
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/429046
; PRIOR FILING DATE: 2002-11-22
```

```
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-718-948-20

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1134 CACCTCCAGCTCCACCT 1150
Db 1 CACCTTCAGGCCACCT 17

RESULT 806
US-60-164-320-14873
; Sequence 14873, Application US/60164320
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley G.
; APPLICANT: Hinkle, Gregory J.
; TITLE OF INVENTION: Xanthomonas campestris Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15804)A
; CURRENT APPLICATION NUMBER: US/60/164,320
; CURRENT FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 18992
; SEQ ID NO 14873
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Xanthomonas campestris
US-60-164-320-14873

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 964 CAACGGTGGAGTCCAA 980
Db 1 CAATGGTGAAGGCCAA 17

RESULT 807
US-60-183-791-14873
; Sequence 14873, Application US/60183791
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley G.
; APPLICANT: Hinkle, Gregory J.
; TITLE OF INVENTION: Xanthomonas campestris Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15804)B
; CURRENT APPLICATION NUMBER: US/60/183,791
; CURRENT FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 18992
; SEQ ID NO 14873
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Xanthomonas campestris
US-60-183-791-14873

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 964 CAACGGTGGAGTCCAA 980
Db 1 CAATGGTGAAGGCCAA 17

RESULT 808
US-10-321-039-630
```

; Sequence 630, Application US/10321039
; GENERAL INFORMATION:
; APPLICANT: Lyamichiev, Victor
; APPLICANT: Lukowiak, Andrew
; APPLICANT: Jarvis, Nancy
; APPLICANT: Kurensky, David
; TITLE OF INVENTION: Amplification Methods and Compositions
; CURRENT APPLICATION NUMBER: US/10/321,039
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/998,157
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/329,113
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/360,489
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 759
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 630
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-321-039-630

Query Match 0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1296 GCCACAGAGCCTGAGACA 1312
|||||
DB 2 GCCACAGAGCCTGGAGA 18

RESULT 809
US-10-354-953-757
; Sequence 757, Application US/10354953
; GENERAL INFORMATION:
; APPLICANT: Dorn, Erin
; APPLICANT: Rasmussen, Eric
; TITLE OF INVENTION: Pharmacogenetic DME Detection Assay Methods and Kits
; FILE REFERENCE: FORS-07810
; CURRENT APPLICATION NUMBER: US/10/354,953
; CURRENT FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 1120
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 757
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-354-953-757

Query Match 0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1296 GCCACAGAGCCTGAGACA 1312
|||||
DB 2 GCCACAGAGCCTGGAGA 18

RESULT 810
PCT-US00-13327-46/c
; Sequence 46, Application PC/TUS0013327
; GENERAL INFORMATION:
; APPLICANT: McGrail, Maura
; APPLICANT: Russell, Deanna L.
; APPLICANT: Shattuck, Donna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: DIABETES GENE

; FILE REFERENCE: Diabetes Gene III
; CURRENT APPLICATION NUMBER: PCT/US00/13327
; CURRENT FILING DATE: 2000-05-16
; PRIOR APPLICATION NUMBER: US 60/174,700
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/135,423
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-13327-46

Query Match 0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1263 CCCCTTCAGAGTGGG 1279
|||||
DB 19 CACCTTGAGAGTGGG 3

RESULT 811
PCT-US00-13327-48/c
; Sequence 48, Application PC/TUS0013327
; GENERAL INFORMATION:
; APPLICANT: McGrail, Maura
; APPLICANT: Russell, Deanna L.
; APPLICANT: Shattuck, Donna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: DIABETES GENE
; FILE REFERENCE: Diabetes Gene III
; CURRENT APPLICATION NUMBER: PCT/US00/13327
; CURRENT FILING DATE: 2000-05-16
; PRIOR APPLICATION NUMBER: US 60/174,700
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/135,423
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-13327-48

Query Match 0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1263 CCCCTTCAGAGTGGG 1279
|||||
DB 19 CACCTTGAGAGTGGG 3

RESULT 812
PCT-US02-25943-36695
; Sequence 36695, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 36695
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:

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; LOCATION: (3597227)...(3597245)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 39327
PCT-US02-25943-36695

Query Match
Best Local Similarity 0.6%; Score 13.8; DB 1; Length 19;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1087 GGCTTCACCCACCCT 1103
    ||||| |||||
Db 2 GGCTTCATCGCACCT 18

RESULT 813
PCT-US03-05045-87/c
; Sequence 87, Application PC/TUS0305045
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Jamison, Sharon
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor
; FILE REFERENCE: 400/081 (MBHB 02-468-B)
; CURRENT APPLICATION NUMBER: PCT/US03/05045
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/251,117
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 10/277,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/277,494
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 09/916,466
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1263
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 87
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA sense
PCT-US03-05045-87

Query Match
Best Local Similarity 0.6%; Score 13.8; DB 1; Length 19;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1112 GTCCCGTCCCACTTCC 1128
    ||||| |||||
Db 19 GTCCACTGCCCACTTCC 3

RESULT 814
PCT-US03-05045-90/c
; Sequence 90, Application PC/TUS0305045
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics Inc.
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; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Jamison, Sharon
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor;
; FILE REFERENCE: 400/081 (MBHB 02-468-B)
; CURRENT APPLICATION NUMBER: PCT/US03/05045
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/251,117
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/277,494
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 09/916,466
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1263
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA sense
PCT-US03-05045-90

Query Match
Best Local Similarity 0.6%; Score 13.8; DB 1; Length 19;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 739 CAGAACACCGTGTGCAC 755
    ||||| |||||
Db 17 CAGGCACCGTGTGCAC 1

RESULT 815
PCT-US03-05045-336
; Sequence 336, Application PC/TUS0305045
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Jamison, Sharon
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor;
; FILE REFERENCE: 400/081 (MBHB 02-468-B)
; CURRENT APPLICATION NUMBER: PCT/US03/05045
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/251,117
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/277,494
; PRIOR FILING DATE: 2002-10-21
```


APPLICANT: Sina Therapeutics Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
APPLICANT: Pavco, Pamela
APPLICANT: Fosnaugh, Kathy
APPLICANT: Jamison, Sharon
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor
FILE REFERENCE: 400/081 (WBHB 02-468-B)
CURRENT APPLICATION NUMBER: PCT/US03/05045
CURRENT FILING DATE: 2003-05-07
PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US 10/251,117
PRIOR FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 10/163,552
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 10/277,494
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US 09/916,466
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: PCT/US 02/16840
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1263
SOFTWARE: PatentIn version 3.2
SEQ ID NO 831
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: sRNA antisense region
PCT-US03-05045-831

Query Match 0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 5.3e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 858 TGTTAAGGCGACTGAGG 874
Db 3 UGUUGAGGCGCAUGAGG 19
||: |||||: |||||

RESULT 819
US-09-573-425-46/c
Sequence 46, Application US/09573425
GENERAL INFORMATION:
APPLICANT: McGrail, Maura
APPLICANT: Russell, Deanna L.
APPLICANT: Shattuck, Donna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: DIABETES GENE
FILE REFERENCE: Diabetes Gene III
CURRENT APPLICATION NUMBER: US/09/573,425
CURRENT FILING DATE: 2000-05-16
PRIOR APPLICATION NUMBER: US 60/174,700
PRIOR FILING DATE: 2000-01-06
PRIOR APPLICATION NUMBER: US 60/135,423
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens

US-09-573-425-46

Query Match 0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1263 CCCCTTCAGAGTGGG 1279
Db 19 CACCTTGGAGAGTGGG 3
|||||

RESULT 820
US-09-573-425-48/c
Sequence 48, Application US/09573425
GENERAL INFORMATION:
APPLICANT: McGrail, Maura
APPLICANT: Russell, Deanna L.
APPLICANT: Shattuck, Donna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: DIABETES GENE
FILE REFERENCE: Diabetes Gene III
CURRENT APPLICATION NUMBER: US/09/573,425
CURRENT FILING DATE: 2000-05-16
PRIOR APPLICATION NUMBER: US 60/174,700
PRIOR FILING DATE: 2000-01-06
PRIOR APPLICATION NUMBER: US 60/135,423
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 48
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
US-09-573-425-48

Query Match 0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1263 CCCCTTCAGAGTGGG 1279
Db 19 CACCTTGGAGAGTGGG 3
|||||

RESULT 821
US-10-016-490C-24/c
Sequence 24, Application US/10016490C
GENERAL INFORMATION:
APPLICANT: Yin, James Q.
TITLE OF INVENTION: Methods for design and selection of short double-stranded
FILE REFERENCE: 01-2793
CURRENT APPLICATION NUMBER: US/10/016,490C
CURRENT FILING DATE: 2002-11-22
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: The same as those in human.
US-10-016-490C-24

Query Match 0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1108 TTGAGTCCGTCGACAG 1124
Db 17 TTCAGTTCGTCGACAG 1
|||||


```
;
; FEATURE:
; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-46529

Query Match          0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1134 CACCTCCAGCTCCACCT 1150
      |||||
Db 19 CTCCTCCAGCTCCAACT 3

RESULT 830
US-10-293-338-6274
; Sequence 6274, Application US/10293338
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE REFERENCE: 45282
; CURRENT APPLICATION NUMBER: US/10/293,338
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 8785
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6274
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-338-6274

Query Match          0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 750 GTGCACCTGCCATGCAG 766
      |||||
Db 1 GTGCGCTGCCAGGCAG 17

RESULT 831
US-10-303-778-12689
; Sequence 12689, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12689
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-12689

Query Match          0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 918 TCTTTCCTTTTATCCC 934
      |||||
Db 2 TCTTTCCTTTTATCCC 18

RESULT 832
US-10-310-188-1678/c
; Sequence 1678, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENH
```

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;
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1678
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-1678

Query Match          0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1244 CCTCCGACCCCATCCC 1260
      |||||
Db 17 CCTCAGACACCATCCC 1

RESULT 833
US-10-310-188-6272
; Sequence 6272, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GI
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6272
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-6272

Query Match          0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1099 ACCCTGGCTTCAGTCC 1115
      |||||
Db 2 ACCCTGGCTTCAGGCC 18

RESULT 834
US-10-310-188-10574/c
; Sequence 10574, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10574
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-10574

Query Match          0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1243 GCCTCCGACCCCATCCC 1259
      |||||
Db 18 GCCTCCGACCCCATCCC 2
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RESULT 835
US-10-310-188-18123/c
; Sequence 18123, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18123
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-18123

Query Match          0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1245 CTCGACCCCATCCCA 1261
    ||||| ||||| |||||
DB 17 CTCGACCCCATCCCA 1

RESULT 836
US-10-310-188-23028
; Sequence 23028, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23028
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-23028

Query Match          0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 918 TCCTTTCCTTTTATCCC 934
    ||||| ||||| |||||
DB 2 TCCTTTCCTTTTATCCC 18

RESULT 837
US-10-310-188-33554
; Sequence 33554, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33554
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-33554

Query Match          0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1245 CTCGACCCCATCCCA 1261
    ||||| ||||| |||||
DB 17 CTCGACCCCATCCCA 1

RESULT 838
US-10-310-188-34905/c
; Sequence 34905, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34905
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-34905

Query Match          0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1120 CCCATTCCACCTTCAC 1136
    ||||| ||||| |||||
DB 17 CCCATTCCACCTTCAC 1

RESULT 839
US-10-310-188-72813/c
; Sequence 72813, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72813
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-72813

Query Match          0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCAACCCCC 1267
    ||||| ||||| |||||
DB 17 CCCCATCCCCAACCCCC 1

RESULT 840
US-10-310-188-72814/c
; Sequence 72814, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
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Query Match          0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1010 CACCTGAAAAAGAGGG 1026
    ||||| ||||| |||||
DB 1 CACCTGAAAAAGAGAGG 17

RESULT 838
US-10-310-188-34905/c
; Sequence 34905, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34905
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-34905

Query Match          0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1120 CCCATTCCACCTTCAC 1136
    ||||| ||||| |||||
DB 17 CCCATTCCACCTTCAC 1

RESULT 839
US-10-310-188-72813/c
; Sequence 72813, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72813
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-72813

Query Match          0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCAACCCCC 1267
    ||||| ||||| |||||
DB 17 CCCCATCCCCAACCCCC 1

RESULT 840
US-10-310-188-72814/c
; Sequence 72814, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
```

; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72814
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-72814

Query Match 0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCACCCCC 1267
Db 18 CCCCATCCCCACCCCC 2

RESULT 841

US-10-310-188-75577/c
; Sequence 75577, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75577
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-75577

Query Match 0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1239 CCTCGCCTCGGACCCCA 1255
Db 19 CCTCGCCTCGGACCCCA 3

RESULT 842

US-10-310-188-78419/c
; Sequence 78419, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78419
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-78419

Query Match 0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1254 CATCCCCACCCCTTC 1270
Db 19 CCTCCCCACCCCTTC 3

RESULT 843

US-10-367-832A-36695
; Sequence 36695, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 36695
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3597227)...(3597245)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 392
US-10-367-832A-36695

Query Match 0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1087 GGCCTCACCCACCCT 1103
Db 2 GGCCTCACCCACCCT 18

RESULT 844

US-60-216-745-8300/c
; Sequence 8300, Application US/60216745
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Abderrahim, Hadi
; APPLICANT: Dufaire-Gare, Isabelle
; TITLE OF INVENTION: BIALLELIC MARKER MAPS FOR USE IN CONSTRUCTING A HIGH DENSITY...
; FILE REFERENCE: 84 US1,PRO
; CURRENT APPLICATION NUMBER: US/60/216,745
; CURRENT FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 13665
; SOFTWARE: Patent.pn
; SEQ ID NO 8300
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-54711 for SEQ 3769,
US-60-216-745-8300

Query Match 0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 802 AGTAAGTGAAGAAAG 818
Db 18 AGTAAGTGAAGAAAG 2

RESULT 845

US-08-729-043-2
; Sequence 2, Application US/08729043
; GENERAL INFORMATION:
; APPLICANT: Leushner, James
; TITLE OF INVENTION: Method, Composition and Kit for Typing
; TITLE OF INVENTION: Classical HLA Class I Genes
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street Suite 309

CITY: Yorktown
STATE: NY
COUNTRY: US
ZIP: 10598
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,043
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Larson, Marina T.
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN.P-037-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 245-3252
TELEFAX: (914) 962-4330
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 21
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: no
ANTI-SENSE: yes
FRAGMENT TYPE: internal
ORIGINAL SOURCE: human
ORGANISM: human
FEATURE:
OTHER INFORMATION: amplification primer for exons 2 and 3 of
US-08-729-043-2

Query Match 0.6%; Score 13.6; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 6.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2042 GCCCTCTGCTGACACGA 2061
|||
Db 1 GCCCTCTGCGGGAAGCA 20

RESULT 846
PCT-US02-25944-7396
Sequence 7396, Application PC/TUS0225944
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: PCT/US02/25944
CURRENT FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 9208
SOFTWARE: Proprietary
SEQ ID NO 7396
LENGTH: 15
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae complete genome.
FEATURE:
LOCATION: (15497)...(15511)
OTHER INFORMATION: Chromosome =11 Strand = negative ConnectronObjectNumber = 8924
PCT-US02-25944-7396

Query Match 0.6%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 902 TGGTCATTTTCTTTG 916
|||
Db 1 TGTTCATTTTCTTTG 15

RESULT 847
PCT-US02-25944-7448
Sequence 7448, Application PC/TUS0225944
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: PCT/US02/25944
CURRENT FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 9208
SOFTWARE: Proprietary
SEQ ID NO 7448
LENGTH: 15
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae complete genome.
FEATURE:
LOCATION: (641065)...(641079)
OTHER INFORMATION: Chromosome =13 Strand = positive ConnectronObjectNumber = 111
PCT-US02-25944-7448

Query Match 0.6%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 902 TGGTCATTTTCTTTG 916
|||
Db 1 TGTTCATTTTCTTTG 15

RESULT 848
US-10-227-564-7396
Sequence 7396, Application US/10227564
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/227,564
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 9208
SOFTWARE: Proprietary
SEQ ID NO 7396
LENGTH: 15
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae complete genome.
FEATURE:
LOCATION: (15497)...(15511)
OTHER INFORMATION: Chromosome =11 Strand = negative ConnectronObjectNumber = 8;
US-10-227-564-7396

Query Match 0.6%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 902 TGGTCATTTTCTTTG 916
|||
Db 1 TGTTCATTTTCTTTG 15

RESULT 849
US-10-227-564-7448
Sequence 7448, Application US/10227564
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/227,564
CURRENT FILING DATE: 2002-08-26

```
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 7448
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (641065)...(641079)
; OTHER INFORMATION: Chromosome = 13 Strand = positive ConnectronObjectNumber = 11860
US-10-287-787-10375/c
Query Match 0.6%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 902 TGGTCATTTCCTTG 916
Db 1 TGTTCATTTCCTTG 15
RESULT 850
US-10-287-787-10375/c
; Sequence 10375, Application US/10287787
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Caulobacter crescentus complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,787
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 27958
; SOFTWARE: Proprietary
; SEQ ID NO 10375
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Caulobacter crescentus complete genome.
; FEATURE:
; LOCATION: (1427129)...(1427143)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 11378
US-10-287-787-10375
Query Match 0.6%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1097 CCACCTGGGCTTCA 1111
Db 15 CCGCCCTGGGCTTCA 1
RESULT 851
US-10-287-787-11243/c
; Sequence 11243, Application US/10287787
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Caulobacter crescentus complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,787
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 27958
; SOFTWARE: Proprietary
; SEQ ID NO 11243
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Caulobacter crescentus complete genome.
; FEATURE:
; LOCATION: (1604124)...(1604138)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 12384
US-10-287-787-11243
Query Match 0.6%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1097 CCACCTGGGCTTCA 1111
Db 15 CCGCCCTGGGCTTCA 1
RESULT 852
PCT-US02-25940-3485
; Sequence 3485, Application PC/TUS0225940
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25940
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 3485
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (437846)...(437861)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 4
PCT-US02-25940-3485
Query Match 0.6%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1235 CAGCCCTCGCCTCCG 1249
Db 1 CAGCCCTCGCCTCCG 15
RESULT 853
PCT-US03-40978-73653/c
; Sequence 73653, Application PC/TUS0340978
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: PCT/US03/40978
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73653
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
PCT-US03-40978-73653
Query Match 0.6%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1132 TTCACCTCCAGCTCC 1145
Db 16 TTCCTCCAGCTCC 2
RESULT 854
US-09-573-684-10/c
; Sequence 10, Application US/09573684
; GENERAL INFORMATION:
; APPLICANT: HOVANEC, TIMOTHY A.
; APPLICANT: BURRELL, PAUL C.
; TITLE OF INVENTION: AMMONIA-OXIDIZING BACTERIA
; FILE REFERENCE: 81289/264667/ASH
; CURRENT APPLICATION NUMBER: US/09/573,684
; CURRENT FILING DATE: 2000-05-14
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.1
```

; SEQ ID NO 10
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-573-684-10

Query Match 0.6%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1184 CCGCAGAGAGGTGG 1198
||||| |||||
Db 15 CCGCGYAGAGGTGG 1

RESULT 855
US-10-227-563-3485
; Sequence 3485, Application US/10227563
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,563
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 3485
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (437846)...(437861)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 4094
US-10-227-563-3485

Query Match 0.6%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1235 CAGCCCTCGCCTCCG 1249
||||| |||||
Db 1 CAGCCCTCGCGCGC 15

RESULT 856
US-10-294-040-85/c
; Sequence 85, Application US/10294040
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Helicobacter pylori 26695 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,040
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1102
; SOFTWARE: Proprietary
; SEQ ID NO 85
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Helicobacter pylori 26695 complete genome.
; FEATURE:
; LOCATION: (137511)...(137526)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 135
US-10-294-040-85

Query Match 0.6%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 907 ATTTCCTTGGCTT 921
||||| |||||
Db 15 ATTTCCTTGGCTT 1

RESULT 857
US-10-310-188-78695/c
; Sequence 78695, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GI
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47497
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78695
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-78695

Query Match 0.6%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1244 CCTCCGACCCCATCC 1258
||||| |||||
Db 15 CCTCCACCCCATCC 1

RESULT 858
US-10-367-892-3485
; Sequence 3485, Application US/10367892
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,892
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 3485
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (437846)...(437861)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 4
US-10-367-892-3485

Query Match 0.6%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1235 CAGCCCTCGCCTCCG 1249
||||| |||||
Db 1 CAGCCCTCGCGCGC 15

RESULT 859
US-10-659-948A-10/c
; Sequence 10, Application US/10659948A
; GENERAL INFORMATION:
; APPLICANT: Hovavac, Timothy A
; TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-294309
; CURRENT APPLICATION NUMBER: US/10/659,948A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19

Qy 907 ATTTCTTTGGCTT 921
|:::|::|::|::
db 3 AUUUUUUUUGUCUU 17

```

RESULT 864
US-09-531-025A-1602
; Sequence 1602, Application US/09531025A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Ken
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MHB00-845-E (247/277)
; CURRENT APPLICATION NUMBER: US/09/531,025A
; CURRENT FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6341
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1602
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-531-025A-1602

```

```
Query Match          0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. NO. 5.5e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;
```

Qy 909 TTTCCTTTGGTCTTTG 923
:::|:::|:::|
Db 1 UUUUUUUUGUUNUG 15

```

RESULT 865
US-09-541-946-1657/c
; Sequence 1657, Application US/09541946
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Altshuler, David M.
; APPLICANT: Ireland, James S.
; APPLICANT: Sklar, Pamela
; APPLICANT: Patil, Nila
; APPLICANT: Lipschutz, Robert J.
; APPLICANT: Daley, George Q.
; TITLE OF INVENTION: CHARACTERIZATION OF SINGLE NUCLEOTIDE
; POLYMORPHISMS IN CODING REGIONS OF HUMAN GENES
; FILE REFERENCE: 2825.1017-003
; CURRENT APPLICATION NUMBER: US/09/541,946
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,248
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2889
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1657
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-541-946-1657

```

```
Query Match          0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 1073 TCAGTCCCACTCCAG 1087
db 15 TGAGTCCCACTCCAG 1

```

RESULT 866
US-09-541-946-1659/c
; Sequence 1659, Application US/09541946
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Altshuler, David M.
; APPLICANT: Ireland, James S.
; APPLICANT: Sklar, Pamela
; APPLICANT: Patil, Nilal
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Daley, George Q.
; TITLE OF INVENTION: CHARACTERIZATION OF SINGLE NUCLEOTIDE
; POLYMORPHISMS IN CODING REGIONS OF HUMAN GENES
; FILE REFERENCE: 2825.1017-003
; CURRENT APPLICATION NUMBER: US/09/541,946
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,248
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2889
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1659
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-541-946-1659

```

```
Query Match          0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 1073 TCAGTCCCACTCCAG 1087
 Db 15 TGAGTCCCACTCCAG 1

```

RESULT 867
US-09-546-745A-6637
; Sequence 6637, Application US/09546745A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: Zwack, Michael
; APPLICANT: Pavco, Pam
; APPLICANT: MCSwigen, Jim
; TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules
; FILE REFERENCE: 237/193
; CURRENT APPLICATION NUMBER: US/09/546, 745A
; CURRENT FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 7043
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6637
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-546-745A-6637

Query Match          0.6%   Score 13.4;   DB 1;   Length 17;
Best Local Similarity 73.3%   Pred. No. 5.5e+02;

```

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 73.3%; Pred. No. 5.5e+02;

OTHER INFORMATION: Oligonucleotide primer
US-09-541-946-1657

Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1065 CCCAGCTTCAGTCC 1079
Db 1 CCCAGCTTCAGTCC 15
|||||:|:|:|

RESULT 868
US-09-572-021-1505/C
; Sequence 1505, Application US/09572021
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, Jim
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McLaughlin, Fiona
; APPLICANT: Randall, Anna Maria
; TITLE OF INVENTION: Method and Reagent for the Inhibition of ERG
; FILE REFERENCE: 249/006
; CURRENT APPLICATION NUMBER: US/09/572,021
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 5366
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1505
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-572-021-1505

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 752 GCACCTGCCATGCG 766
Db 16 GCACCTGCCATGCG 2
|||||:|:|:|

RESULT 869
US-09-636-385-909
; Sequence 909, Application US/09636385
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-F (250/125)
; CURRENT APPLICATION NUMBER: US/09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6341
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 909
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-09-636-385-909

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 907 ATTTCTTGTGCTT 921
|:|:|:|:|:|:|:|:|

Db 3 AUUUUUUUUUUUU 17

RESULT 870
US-09-636-385-1602
; Sequence 1602, Application US/09636385
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-F (250/125)
; CURRENT APPLICATION NUMBER: US/09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6341
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1602
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-09-636-385-1602

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 909 TTCTTTGTGCTTGTG 923
|:|:|:|:|:|:|:|:|
Db 1 UUUUUUUUUUUU 15

RESULT 871
US-09-696-347-909
; Sequence 909, Application US/09696347
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Ken
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/001
; CURRENT APPLICATION NUMBER: US/09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6389
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 909
; LENGTH: 17
; TYPE: RNA

```
; ORGANISM: Hepatitis B Virus
US-09-696-347-903

Query Match
Best Local Similarity 0.6%; Score 13.4; DB 1; Length 17;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 907 ATTCTTTGCTTGT 921
Db 3 AUUUUUUUUUUUU 17

RESULT 872
US-09-696-347-1602
; Sequence 1602, Application US/09696347
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Ken
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/001
; CURRENT APPLICATION NUMBER: US/09/696,347
; CURRENT FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 07/982,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6389
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1602
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-09-696-347-1602

Query Match
Best Local Similarity 0.6%; Score 13.4; DB 1; Length 17;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 909 TTCTTTGCTTGT 923
Db 1 UUUUUUUUUUUU 15

RESULT 873
US-09-780-533A-1806/c
; Sequence 1806, Application US/09780533A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowirra, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
```

```
; SEQ ID NO 1806
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1806

Query Match
Best Local Similarity 0.6%; Score 13.4; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1135 ACCTCCAGCTCCAC 1149
Db 17 ACCTCCAGCTCCCTC 3

RESULT 874
US-09-780-533A-2377/c
; Sequence 2377, Application US/09780533A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowirra, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2377
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2377

Query Match
Best Local Similarity 0.6%; Score 13.4; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1134 CACCTCCAGCTCCAC 1148
Db 15 CACCTCCAGCTCCTC 1

RESULT 875
US-09-818-875-559/c
; Sequence 559, Application US/09818875
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,530
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 559
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
```

US-09-818-875-559

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 953 TGTATCGCTACCAAC 967
|||||
Db 15 TGTATCGCTACCAAC 1

RESULT 876

US-09-818-875-560
; Sequence 560, Application US/09818875
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,999
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 560
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-875-560

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 953 TGTATCGCTACCAAC 967
|||||
Db 3 TGTATCGCTACCAAC 17

RESULT 877

US-09-877-478-909
; Sequence 909, Application US/09877478
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MEHB00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 10060830
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1602
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-1602

; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 909
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-909

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 907 ATTTCTTTGGTCTT 921
|:::|:::|:::
Db 3 AUUUCUUUGUCUU 17

RESULT 878

US-09-877-478-1602
; Sequence 1602, Application US/09877478
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MEHB00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1602
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-1602

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 909 TTTCTTTGGTCTTG 923
|:::|:::|:::
Db 1 UUUUUUUUGUCUU 15

RESULT 879
US-10-060-830-203
; Sequence 203, Application US/10060830
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Nguyen, Cung-Tuong

;; TITLE OF INVENTION: HUMAN LCCL DOMAIN CONTAINING PROTEIN
;; FILE REFERENCE: PB0169
;; CURRENT APPLICATION NUMBER: US/10/060,830
;; CURRENT FILING DATE: 2002-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 09/864,761
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/325,062
;; PRIOR FILING DATE: 2001-09-25
;; NUMBER OF SEQ ID NOS: 1123
;; SOFTWARE: Acomica Sequence Listing Engine
;; SEQ ID NO 203
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-060-830-203

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 879 AGGCACACAGTGCT 893
DB 3 AGTCACACAGTGCT 17

RESULT 880
US-10-060-830-206
;; Sequence 206, Application US/10060830
;; GENERAL INFORMATION:
;; APPLICANT: Nguyen, Hung-Tuong
;; TITLE OF INVENTION: HUMAN LCCL DOMAIN CONTAINING PROTEIN
;; FILE REFERENCE: PB0169
;; CURRENT APPLICATION NUMBER: US/10/060,830
;; CURRENT FILING DATE: 2002-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 09/864,761
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/325,062
;; PRIOR FILING DATE: 2001-09-25
;; NUMBER OF SEQ ID NOS: 1123
;; SOFTWARE: Acomica Sequence Listing Engine
;; SEQ ID NO 206
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-060-830-206

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 880 GCACACAGTGCTG 894
DB 1 GTCACACAGTGCTG 15

RESULT 881
US-10-209-787-559/c
;; Sequence 559, Application US/10209787
;; GENERAL INFORMATION:
;; APPLICANT: Kmiec, Eric B.
;; APPLICANT: Gamper, Howard B.
;; APPLICANT: Rice, Michael C.
;; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
;; TITLE OF INVENTION: Stranded Oligonucleotides
;; FILE REFERENCE: Napro-4
;; CURRENT APPLICATION NUMBER: US/10/209,787
;; CURRENT FILING DATE: 2002-07-30
;; PRIOR APPLICATION NUMBER: US 09/818,875
;; PRIOR FILING DATE: 2001-03-27
;; PRIOR APPLICATION NUMBER: US 60/192,176
;; PRIOR FILING DATE: 2000-03-27
;; PRIOR APPLICATION NUMBER: US 60/192,179
;; PRIOR FILING DATE: 2000-03-27
;; PRIOR APPLICATION NUMBER: US 60/208,538
;; PRIOR FILING DATE: 2000-06-01
;; PRIOR APPLICATION NUMBER: US 60/244,989
;; PRIOR FILING DATE: 2000-10-30
;; NUMBER OF SEQ ID NOS: 4385
;; SOFTWARE: Friedman macro Napro4
;; SEQ ID NO 559
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-209-787-559

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 953 TGATCGCTACCAAC 967
DB 15 TGATCGCTACCAAC 1

RESULT 882
US-10-209-787-560
;; Sequence 560, Application US/10209787
;; GENERAL INFORMATION:
;; APPLICANT: Kmiec, Eric B.
;; APPLICANT: Gamper, Howard B.
;; APPLICANT: Rice, Michael C.
;; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
;; TITLE OF INVENTION: Stranded Oligonucleotides
;; FILE REFERENCE: Napro-4
;; CURRENT APPLICATION NUMBER: US/10/209,787
;; CURRENT FILING DATE: 2002-07-30
;; PRIOR APPLICATION NUMBER: US 09/818,875
;; PRIOR FILING DATE: 2001-03-27
;; PRIOR APPLICATION NUMBER: US 60/192,176
;; PRIOR FILING DATE: 2000-03-27
;; PRIOR APPLICATION NUMBER: US 60/192,179
;; PRIOR FILING DATE: 2000-03-27
;; PRIOR APPLICATION NUMBER: US 60/208,538
;; PRIOR FILING DATE: 2000-06-01
;; PRIOR APPLICATION NUMBER: US 60/244,989
;; NUMBER OF SEQ ID NOS: 4385
;; SOFTWARE: Friedman macro Napro4
;; SEQ ID NO 560
;; LENGTH: 17
;; TYPE: DNA

```
; ORGANISM: Homo sapiens
US-10-209-787-560

Query Match          0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 953 TGTATCGCTACCAAC 967
Db 3 TGTATCGCTACCAAC 17

RESULT 883
US-10-261-185-559/c
; Sequence 559, Application US/102611185
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 559
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-261-185-559

Query Match          0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 953 TGTATCGCTACCAAC 967
Db 15 TGTATCGCTACCAAC 1

RESULT 884
US-10-261-185-560
; Sequence 560, Application US/102611185
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
```

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; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 560
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-261-185-560

Query Match          0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 953 TGTATCGCTACCAAC 967
Db 3 TGTATCGCTACCAAC 17

RESULT 885
US-10-310-188-37271
; Sequence 37271, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GI
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37271
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-37271

Query Match          0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 865 GGCATCTGAGGACTCA 879
Db 2 GGCATCTGAGGACTCA 16

RESULT 886
US-10-339-782-328
; Sequence 328, Application US/10339782
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Goodman, Laurie J
; APPLICANT: Bowen, Benjamin A
; TITLE OF INVENTION: Identification of Specific Biomarkers for Breast Cancer Cells
; FILE REFERENCE: 37-0001100S
; CURRENT APPLICATION NUMBER: US/10/339,782
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 328
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-782-328

Query Match          0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1091 TCAGCCCCCACCCTGG 1105
Db 3 TCAGCCCCCACCCTGG 17

RESULT 887
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```
US-10-342-902-909
; Sequence 909, Application US/10342902
; GENERAL INFORMATION:
; APPLICANT: Sina Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MHB00-845-1)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 07/982,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6592
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 909
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-10-342-902-909

Query Match          0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 907 ATTTCCTTGGTCTT 921
Db 3 AUUUUUUUUUUUUU 17

RESULT 888
US-10-342-902-1602
; Sequence 1602, Application US/10342902
; GENERAL INFORMATION:
; APPLICANT: Sina Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MHB00-845-1)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 07/982,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6592
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1602
```

```
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-10-342-902-1602

Query Match          0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 909 TTTCCTTGGTCTTGG 923
Db 1 UUUUUUUUUUUUUU 15

RESULT 889
US-10-623-107-559/c
; Sequence 559, Application US/10623107
; GENERAL INFORMATION:
; APPLICANT: KMEC, ERIC B.
; TITLE OF INVENTION: TARGETED NUCLEIC ACID SEQUENCE ALTERATION USING PLURAL
; FILE REFERENCE: NAPRO-14 US
; CURRENT APPLICATION NUMBER: US/10/623,107
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/397,555
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: PatentIn ver 3.2
; SEQ ID NO 559
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-623-107-559

Query Match          0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 953 TGTATCGCTACCAAC 967
Db 15 TGTATCGCTACCAAC 1

RESULT 890
US-10-623-107-560
; Sequence 560, Application US/10623107
; GENERAL INFORMATION:
; APPLICANT: KMEC, ERIC B.
; TITLE OF INVENTION: TARGETED NUCLEIC ACID SEQUENCE ALTERATION USING PLURAL
; FILE REFERENCE: NAPRO-14 US
; CURRENT APPLICATION NUMBER: US/10/623,107
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/397,555
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: PatentIn ver 3.2
; SEQ ID NO 560
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-623-107-560

Query Match          0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 953 TGTATCGCTACCAAC 967
Db 3 TGTATCGCTACCAAC 17

RESULT 891
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```
US-10-669-841-909
; Sequence 909, Application US/10669841
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS B VIRUS REPLICATION
; FILE REFERENCE: 400/042US (MBHB02-249-E)
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 909
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-909

Query Match      0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 907 ATTTCTTTGGCTT 921
Db 3 AUUUUUUUUUUUUU 17

RESULT 892
US-10-669-841-1602
; Sequence 1602, Application US/10669841
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS B VIRUS REPLICATION
; FILE REFERENCE: 400/042US (MBHB02-249-E)
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 909
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-909

Query Match      0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 907 ATTTCTTTGGCTT 921
Db 3 AUUUUUUUUUUUUU 17

RESULT 892
US-10-669-841-1602
; Sequence 1602, Application US/10669841
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS B VIRUS REPLICATION
; FILE REFERENCE: 400/042US (MBHB02-249-E)
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 909
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-1602

Query Match      0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 909 TTCTTTGGCTTTG 923
Db 1 UUUUUUUUUUUUUU 15

RESULT 893
US-10-681-074-559/c
; Sequence 559, Application US/10681074
; GENERAL INFORMATION:
; APPLICANT: KMEC, ERIC B.
; APPLICANT: VAN BRABANT, ANJA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION
; FILE REFERENCE: Napro-18 US
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: US 60/453,360
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/416,983
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 4375
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 559
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-681-074-559

Query Match      0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 953 TGTATCGCTACCAAC 967
Db 15 TGTATCGCTACCAAC 1

RESULT 894
US-10-681-074-560
; Sequence 560, Application US/10681074
```

GENERAL INFORMATION:
APPLICANT: KMEC, ERIC B.
APPLICANT: VAN BRABANT, ANJA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN
FILE OF INVENTION: OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION
FILE REFERENCE: Napro-18 US
CURRENT APPLICATION NUMBER: US/10/681,074
CURRENT FILING DATE: 2003-10-07
PRIOR APPLICATION NUMBER: US 60/453,360
PRIOR FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: US 60/416,983
PRIOR FILING DATE: 2002-10-07
NUMBER OF SEQ ID NOS: 4375
SOFTWARE: PatentIn version 3.2
SEQ ID NO 560
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-10-681-074-560

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 953 TGTATCGCTACCAAC 967
|||||
Db 3 TGTATCGCTACCAAC 17

RESULT 895
US-10-723-361-973
Sequence 973, Application US/10723361
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
FILE REFERENCE: PB0105
CURRENT APPLICATION NUMBER: US/10/723,361
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US 09/866,108
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 973
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-10-723-361-973

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1056 GGCCCCAACCCCAAG 1070
|||||
Db 2 GGCCCCAACCCCAAG 16

RESULT 896
US-10-723-361-974
Sequence 974, Application US/10723361
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART
FILE REFERENCE: PB0105
CURRENT APPLICATION NUMBER: US/10/723,361
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US 09/866,108
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 974
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-10-723-361-974

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1056 GGCCCCAACCCCAAG 1070
|||||
Db 1 GGCCCCAACCCCAAG 15

RESULT 897
US-10-741-600-73370/c
Sequence 73370, Application US/10741600
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73370
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-110-741-600-73370

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1133 TCACCTCCAGCTCCA 1147
| | | | | | | | | | | | | | | | | | | | | |
Db 15 TCACCTGCAGCTCCA 1

RESULT 898
US-60-325-062-203
; Sequence 203, Application US/60325062

; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: HUMAN LCCL_DOMAN CONTAINING PROTEIN
; FILE REFERENCE: AROMICA-22
; CURRENT APPLICATION NUMBER: US/60/325,062
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 1123
; SOFTWARE: Aromica Sequence Listing Engine
; SEQ ID NO 203
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-325-062-203

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 879 AGGCACACAGTGCT 893
| | | | | | | | | | | | | | | | | | | | | |
Db 3 AGTCACACAGTGCT 17

RESULT 899
US-60-325-062-206
; Sequence 206, Application US/60325062

; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: HUMAN LCCL_DOMAN CONTAINING PROTEIN
; FILE REFERENCE: AROMICA-22
; CURRENT APPLICATION NUMBER: US/60/325,062
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 1123
; SOFTWARE: Aromica Sequence Listing Engine
; SEQ ID NO 206
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-325-062-206

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 880 GGCACACAGTGCTG 894
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GTCACACAGTGCTG 15

RESULT 900
PCT-US02-00985-19/c
; Sequence 19, Application PC/TUS0200985

; GENERAL INFORMATION:
; APPLICANT: Yissum Research Development Company of The Hebrew University of Jerusalem
; APPLICANT: Yissum Research Development Company of The Hebrew University of Jerusalem
; TITLE OF INVENTION: NANOPARTICLES CONTAINING POLYMERIC NUCLEIC ACID HOMOLOGS,
; TITLE OF INVENTION: PHARMACEUTICAL....
; FILE REFERENCE: 325/87
; CURRENT APPLICATION NUMBER: PCT/US02/00985
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/335,837
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Mus musculus
PCT-US02-00985-19

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1096 CCCACCTGGGCTTC 1110
| | | | | | | | | | | | | | | | | | | | | |
Db 17 CCCACATGGGCTTC 3

RESULT 901
PCT-US02-24115-32/c
; Sequence 32, Application PC/TUS0224115

; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TOLAND, Amanda E.
; APPLICANT: BALMAIN, Allan
; TITLE OF INVENTION: STK15 (STK6) GENE POLYMORPHISM AND METHODS OF DETERMINING CANC
; FILE REFERENCE: UCSE1120-2W0
; CURRENT APPLICATION NUMBER: PCT/US02/24115
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/334,146
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/308,911
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32

```
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Amplification reaction primer
PCT-US02-24115-32

Query Match          0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1093 ACCCCACCTGGGC 1107
Db 15 ACCCTCACCTGGGC 1

RESULT 902
PCT-US02-25940-18207
; Sequence 18207, Application PC/TUS0225940
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25940
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 18207
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (2199746)...(2199763)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 21297
PCT-US02-25940-18207

Query Match          0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1055 TGGCCCCCAACCCAA 1069
Db 4 TGGCCCCCAACCCAA 18

RESULT 903
PCT-US02-34679-162/c
; Sequence 162, Application PC/TUS0234679
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampeon, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308PC
; CURRENT APPLICATION NUMBER: PCT/US02/34679
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
```

```
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
PCT-US02-34679-162

Query Match          0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 812 AGAAAAGCCTGGAGT 826
Db 16 AGAGAAGCCTGGAGT 2

RESULT 904
PCT-US03-07585-40
; Sequence 40, Application PC/TUS0307585
; GENERAL INFORMATION:
; APPLICANT: Holland-Staley, Carol
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: IDENTIFYING AND CHARACTERIZING HEPATITIS C
; FILE REFERENCE: PCV-001PC
; CURRENT APPLICATION NUMBER: PCT/US03/07585
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 60/363,603
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
PCT-US03-07585-40

Query Match          0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1056 GGCCCCCAACCCAAAG 1070
Db 4 GGCCCCCAACCCAAAG 18

RESULT 905
PCT-US02-00985-19/c
; Sequence 19, Application PC/TIL0200985
; GENERAL INFORMATION:
; APPLICANT: Yissum Research Development Company of The Hebrew University of Jerusalem
; TITLE OF INVENTION: YISSUM RESEARCH DEVELOPMENT COMPANY OF THE HEBREW UNIVERSITY OF JERUSALEM
; TITLE OF INVENTION: NANOPARTICLES CONTAINING POLYMERIC NUCLEIC ACID HOMOLOGS,
; FILE REFERENCE: 325/87
; CURRENT APPLICATION NUMBER: PCT/IL02/00985
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 60/335,837
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Mus musculus
```

PCT-IL02-00985-19

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1096 CCCACCTGGGCTTC 1110
|||||
Db 17 CCCACCATGGGCTTC 3

RESULT 906

US-09-155-885A-270/c

; Sequence 270, Application US/09155885A

; GENERAL INFORMATION:

; APPLICANT: STUYVER, LIEVEN

; ROSSAU, RUDI

; MAERTENS, GEERT

; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV

; NUMBER OF SEQUENCES: 313

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/155,885A

; FILING DATE: 08-Oct-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/EP97/02002

; FILING DATE: 21-APR-1997

; APPLICATION NUMBER: EP 96870053.4

; FILING DATE: 19-APR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: SADOFF, B.J.

; REGISTRATION NUMBER: 36,663

; REFERENCE/DOCKET NUMBER: 2551-5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4000

; TELEFAX: (703) 816-4100

; INFORMATION FOR SEQ ID NO: 270:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; SEQUENCE DESCRIPTION: SEQ ID NO: 270:

US-09-155-885A-270

Query Match

0.6%; Score 13.4; DB 1; Length 18;

Best Local Similarity 93.3%; Pred. No. 5.8e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
|||||
Db 18 GCCAAGAGAAACAGA 4

RESULT 907

US-09-155-885A-272/c

; Sequence 272, Application US/09155885A

; GENERAL INFORMATION:

APPLICANT: STUYVER, LIEVEN
ROSSAU, RUDI
MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 272:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 272:
US-09-155-885A-272

Query Match 0.8%; Score 13.4; DB 1; Length 18;

Best Local Similarity 93.3%; Pred. No. 5.8e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
|||||
Db 18 GCCATGAGAAACAGA 4

RESULT 908

US-09-155-885A-273/c

; Sequence 273, Application US/09155885A

; GENERAL INFORMATION:

; APPLICANT: STUYVER, LIEVEN

; ROSSAU, RUDI

; MAERTENS, GEERT

; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV

; NUMBER OF SEQUENCES: 313

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 273:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 273:
US-09-155-885A-273

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
Db 18 GCCAGGAGAAACGGA 4

RESULT 909
US-09-857-278-18
Sequence 18, Application US/09857278
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J Ackermann
APPLICANT: Lex M. Cowser
TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-1
FILE REFERENCE: RTSP-0142
CURRENT APPLICATION NUMBER: US/09/857,278
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 09/205,204
PRIOR FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 18
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-857-278-18

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 761 ATGCAGGTTTCTTC 775
Db 4 ATGCAGGCTTCTTC 18

RESULT 910
US-10-108-732-47/c

Sequence 47, Application US/10108732
GENERAL INFORMATION:
APPLICANT: Box, Neil F
APPLICANT: Duffy, David L
APPLICANT: Hayward, Nicholas K
APPLICANT: Martin, Nicholas G
APPLICANT: Sturm, Richard A
APPLICANT: Gruis, Nelske A
APPLICANT: Van Der Velde, Pieter
APPLICANT: Bergman, Wilma
APPLICANT: Frants, Rune R
TITLE OF INVENTION: MELANOMA RISK DETECTION
FILE REFERENCE: 8795-27U1
CURRENT APPLICATION NUMBER: US/10/108,732
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/279,515
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
SEQ ID NO 47
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: hmsHR C-inner sequencing primer 2
US-10-108-732-47

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1133 TCACCTCCAGCTCCA 1147
Db 16 TCACCTCCAGCTCCA 2

RESULT 911
US-10-209-324-32/c
Sequence 32, Application US/10209324
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF CALIFORNIA SAN FRANCISCO
APPLICANT: TOLAND, Amanda E.
APPLICANT: BALMAIN, Allan
TITLE OF INVENTION: STK15 (STK6) GENE POLYMORPHISM AND METHODS OF DETERMINING CANCER
FILE REFERENCE: UCSF120-2
CURRENT APPLICATION NUMBER: US/10/209,324
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: US 60/334,146
PRIOR FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: US 60/308,911
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
SEQ ID NO 32
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Amplification reaction primer
US-10-209-324-32

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1093 ACCCCACCCCTGGC 1107
Db 15 ACCCTCACCTGGC 1

RESULT 912
US-10-227-563-18207
Sequence 18207, Application US/10227563

```
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,563
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 18207
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (2199746)...(2199763)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 21297
US-10-227-563-18207

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1055 TGGCCCAACCCAA 1069
Db 4 TGGCCCAACCCAA 18

RESULT 913
US-10-282-174-162/c
; Sequence 162, Application US/10282174
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gomul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; FILE REFERENCE: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308
; CURRENT APPLICATION NUMBER: US/10/282,174
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-282-174-162

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 812 AGAAAAGCCTGGAGT 826
```

```
Db 16 AGAAGCCTGGAGT 2

RESULT 914
US-10-294-040-54/c
; Sequence 54, Application US/10294040
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Helicobacter pylori 26695 complete genome.
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,040
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1102
; SOFTWARE: Proprietary
; SEQ ID NO 54
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Helicobacter pylori 26695 complete genome.
; FEATURE:
; LOCATION: (101442)...(101459)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber =
US-10-294-040-54

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 907 ATTTCTTTGGTCTT 921
Db 15 ATTTCTTTGGTCTT 1

RESULT 915
US-10-294-040-279/c
; Sequence 279, Application US/10294040
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Helicobacter pylori 26695 complete genome.
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,040
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1102
; SOFTWARE: Proprietary
; SEQ ID NO 279
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Helicobacter pylori 26695 complete genome.
; FEATURE:
; LOCATION: (370226)...(370242)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber =
US-10-294-040-279

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 907 ATTTCTTTGGTCTT 921
Db 15 ATTTCTTTGGTCTT 1

RESULT 916
US-10-310-188-82210/c
; Sequence 82210, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82210
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-82210

Query Match      0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 967 CGGTGGAAGTCCCAAG 981
Db 18 CGGTGGAAGACCAAG 4

RESULT 917
US-10-349-143-5085
; Sequence 5085, Application US/10349143
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET 020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5085
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18__bind
; OTHER INFORMATION: upstream amplification primer 99-20747 for SEQ 1151,
US-10-349-143-5085

Query Match      0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 976 TCCAAAGCTCTACTCC 990
Db 4 TCCAAAGCTCTACTCC 18

RESULT 918
US-10-367-892-18207
; Sequence 18207, Application US/10367892
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,892
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 18207
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (2199746)...(2199763)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 21297
```

US-10-367-892-18207

```
Query Match      0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 1055 TGGCCCCCAACCCAA 1069

Db 4 TGGCCCCCAACCCAA 18

RESULT 919

```
US-10-453-792-270/C
; Sequence 270, Application US/10453792
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; APPLICANT: ROSSAU, RUDI
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 270:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 270:
US-10-453-792-270
```

```
Query Match      0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 728 GCCAGAGAAACAGA 742

Db 18 GCCAGAGAAACAGA 4

RESULT 920

US-10-453-792-272/C

; Sequence 272, Application US/10453792
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 35,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4100
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 272:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 272:
US-10-453-792-272

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
||| |||||
Db 18 GCCATGAGAAACAGA 4

RESULT 921
US-10-453-792-273/c
; Sequence 273, Application US/10453792
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.

; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 273:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 273:
US-10-453-792-273

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
||| |||||
Db 18 GCCAGGAGAAACAGA 4

RESULT 922
US-10-464-158-18
; Sequence 18, Application US/10464158
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-1
; FILE REFERENCE: ISPH-0749
; CURRENT APPLICATION NUMBER: US/10/464,158
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 09/857,278
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/13624
; PRIOR FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: 09/205,204
; PRIOR FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 18
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-464-158-18

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 272:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 272:
US-10-606-879-272

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
Db 18 GCCATGAGAAACAGA 4

RESULT 926
US-10-606-879-273/c
; Sequence 273, Application US/10606879
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/606,879
; FILING DATE: 27-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 273:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 273:
US-10-606-879-273

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
Db 18 GCCAGGAGAAACAGA 4

RESULT 927
US-60-216-745-8219/c
; Sequence 8219, Application US/60216745
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Abderrahim, Hadi
; APPLICANT: Dufaur-Gare, Isabelle
; TITLE OF INVENTION: BIALLELIC MARKER MAPS FOR USE IN CONSTRUCTING A HIGH DENSITY.
; FILE REFERENCE: 84.US1.PRO
; CURRENT APPLICATION NUMBER: US/60/216,745
; CURRENT FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 13665
; SOFTWARE: Patent.pm
; SEQ ID NO 8219
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-53687 for SEQ 3688,
US-60-216-745-8219

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 931 TCCCTCCTCTTCATT 945
Db 15 TCCCTCCTCTTCATT 1

RESULT 928
US-60-492-056-743/c
; Sequence 743, Application US/60492056
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Timothy Vickers
; APPLICANT: C. Frank Bennett
; APPLICANT: Richard H. Griffey
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS AND COMPOSITIONS FOR USE IN MODULATION OF
; FILE REFERENCE: CORE0016US.L
; CURRENT APPLICATION NUMBER: US/60/492,056
; CURRENT FILING DATE: 2003-08-13
; NUMBER OF SEQ ID NOS: 779
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 743
; LENGTH: 18
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-60-492-056-743

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 887 CAGTGTCTGTGCCCC 901
||| ||| ||| ||| ||| |||
DB 15 CAGTGATGTGCCCC 1

RESULT 929
PCT-US00-22029-11/c
; Sequence 11, Application PC/TUS0022029
; GENERAL INFORMATION:
; APPLICANT: KARLSEN, FRANK
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF THE INDICATORS OF
; FILE REFERENCE: 618123-6
; CURRENT APPLICATION NUMBER: PCT/US00/22029
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/149,365
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Escherichia coli
PCT-US00-22029-11

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1227 CCTTGGACAGCCCT 1241
||| ||| ||| ||| ||| |||
DB 19 CCTTGGACAGCCCT 5

RESULT 930
PCT-US03-03473-41
; Sequence 41, Application PC/TUS0303473
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Chowrira, Bharat
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Platelet Derived Growth
; TITLE OF INVENTION: Factor (PDGF) and Platelet Derived Growth Factor Receptor (PDGFR
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 03-073 (400/092)
; CURRENT APPLICATION NUMBER: PCT/US03/03473
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 41
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense
PCT-US03-03473-41

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 6e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1096 CCCACCGTGGCTTC 1110
||| ||| ||| ||| ||| |||
DB 1 CCCACCGTGGCTTC 15

RESULT 931
PCT-US03-03473-352/c
; Sequence 352, Application PC/TUS0303473
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Chowrira, Bharat
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Platelet Derived Growth
; TITLE OF INVENTION: Factor (PDGF) and Platelet Derived Growth Factor Receptor (PDG
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 03-073 (400/092)
; CURRENT APPLICATION NUMBER: PCT/US03/03473
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 352
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
PCT-US03-03473-352

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1096 CCCACCGTGGCTTC 1110
||| ||| ||| ||| ||| |||
DB 19 CCCACCGTGGCTTC 5

RESULT 932
PCT-US03-03662-178/c
; Sequence 178, Application PC/TUS0303662
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Thompson, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Cyclin D1 Gene Express:
PCT-US03-03662-178/c

```
; TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 02-1005-A (400/083)
; CURRENT APPLICATION NUMBER: PCT/US03/03662
; CURRENT FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: US 60/411,275
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 178
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense 1
PCT-US03-03662-178

Query Match          0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 774 TCTAAGAGAAAACGA 788
Db 19 TCTAAGAGAAAACGA 5

RESULT 933
PCT-US03-03662-417
; Sequence 417, Application PC/TUS0303662
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Thompson, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Cyclin D1 Gene Expression
; FILE REFERENCE: 02-1005-A (400/083)
; CURRENT APPLICATION NUMBER: PCT/US03/03662
; CURRENT FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: US 60/411,275
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 417
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense 1
PCT-US03-03662-417

Query Match          0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 774 TCTAAGAGAAAACGA 788
Db 19 TCTAAGAGAAAACGA 5

RESULT 933
PCT-US03-03662-417
; Sequence 417, Application PC/TUS0303662
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Thompson, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Cyclin D1 Gene Expression
; FILE REFERENCE: 02-1005-A (400/083)
; CURRENT APPLICATION NUMBER: PCT/US03/03662
; CURRENT FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: US 60/411,275
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 417
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense 1
PCT-US03-03662-417

Query Match          0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 80.0%; Pred. No. 6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 774 TCTAAGAGAAAACGA 788
Db 1 UCUAAGAGAAAACUA 15

RESULT 934
PCT-US03-04908-231
; Sequence 231, Application PC/TUS0304908
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of BCL2 Gene Expression
; FILE REFERENCE: 02-714-A (400/086)
; CURRENT APPLICATION NUMBER: PCT/US03/04908
; CURRENT FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/396,905
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 882
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 231
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense 1
PCT-US03-04908-231

Query Match          0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 80.0%; Pred. No. 6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 810 TAAGAAAGCCTCGA 824
Db 2 UAAGAAACCUGGA 16

RESULT 935
PCT-US03-04908-645/C
; Sequence 645, Application PC/TUS0304908
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of BCL2 Gene Expression
; FILE REFERENCE: 02-714-A (400/086)
; CURRENT APPLICATION NUMBER: PCT/US03/04908
; CURRENT FILING DATE: 2003-02-18
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; PRIOR APPLICATION NUMBER: US 60/396,905
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 882
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 645
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: s1na antisense region
PCT-US03-04908-645

Query Match          0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 810 TAAGAAAGCCTGGA 824
    |||||
Db 18 TAAGAAAGCCTGGA 4

RESULT 936
PCT-US03-40977-26190/c
; Sequence 26190, Application PC/TUS0340977
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: PCT/US03/40977
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26190
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-40977-26190

Query Match          0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 885 CACAGTGTGCTGCC 899
    |||||
Db 15 CACAGTGTGCTGCC 1

RESULT 937
PCT-US03-40978-73310/c
; Sequence 73310, Application PC/TUS0340978
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: PCT/US03/40978
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73310
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-40978-73310

Query Match          0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 885 CACAGTGTGCTGCC 899
    |||||
Db 15 CACAGTGTGCTGCC 1

RESULT 938
US-08-965-620-775/c
; Sequence 775, Application US/08965620
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Wang, David
; APPLICANT: Hudson, Thomas
; TITLE OF INVENTION: Biallelic Markers
; NUMBER OF SEQUENCES: 3817
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,620
; FILING DATE: 06-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,455
; FILING DATE: 06-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WHI96-10pA (DUP)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 775:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-965-620-775

Query Match          0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1012 CCTGAAAAGAGGGG 1026
    |||||
Db 16 CCTGAAAAGAGGGG 2

RESULT 939
US-09-634-960A-11/c
; Sequence 11, Application US/09634960A
; GENERAL INFORMATION:
```

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; APPLICANT: Karlisen, Frank
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF THE INDICATORS OF CONTAMINATION IN I
; FILE REFERENCE: 5775.018
; CURRENT APPLICATION NUMBER: US/09/634,960A
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/149,365
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-634-960A-11

Query Match      0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1227 CCTTGCACGACCCCT 1241
Db 19 CCCGCGACGACCCCT 5

RESULT 940
US-10-148-687-55
; Sequence 55: Application US/10148687
; GENERAL INFORMATION:
; APPLICANT: WINTER, Gerhard
; APPLICANT: SLADE, Martin Basil
; APPLICANT: WILLIAMS, Keith Leslie
; APPLICANT: GOOLEY, Andrew Arthur
; APPLICANT: Macquarie Research Ltd
; TITLE OF INVENTION: Cryptosporidium sporozoite antigens
; FILE REFERENCE: 047763-5019-US
; CURRENT APPLICATION NUMBER: US/10/148,687
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: PCT/AU00/01492
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: AU P04400
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primers
US-10-148-687-55

Query Match      0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1068 AAGCTTCAGTCCAC 1082
Db 5 AAGCTTCAGTCCAC 19

RESULT 941
US-10-244-647-598
; Sequence 598: Application US/10244647
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceutical, Inc.
; APPLICANT: Morrissey, David
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
; FILE REFERENCE: 400/060 (MBHB02-1000)
```

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; CURRENT APPLICATION NUMBER: US/10/244,647
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: PCT US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 598
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
US-10-244-647-598

Query Match      0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 26.7%; Pred. No. 6e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 909 TTCTTTGGTCTTG 923
Db 1 UUUUUUUUGUUUG 15

RESULT 942
US-10-244-647-637
; Sequence 637: Application US/10244647
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceutical, Inc.
; APPLICANT: Morrissey, David
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
; FILE REFERENCE: 400/060 (MBHB02-1000)
; CURRENT APPLICATION NUMBER: US/10/244,647
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: PCT US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 637
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
US-10-244-647-637

Query Match      0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 26.7%; Pred. No. 6e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 907 ATTTCTTGGTCTT 921
Db 5 AUUUUUUUUGUUU 19

RESULT 943
US-10-244-647-1244/c
; Sequence 1244: Application US/10244647
; GENERAL INFORMATION:
```

APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Morrissey, David
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
FILE REFERENCE: 400/060 (MH02-1000)
CURRENT APPLICATION NUMBER: US/10/244,647
CURRENT FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: PCT US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1244
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-244-647-1244

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 909 TTCTTGTGTCCTTG 923
|||||
Db 19 TTCTTGTGTCCTTG 5

RESULT 944

US-10-244-647-1283/c
Sequence 1283, Application US/10244647
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Morrissey, David
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
FILE REFERENCE: 400/060 (MH02-1000)
CURRENT APPLICATION NUMBER: US/10/244,647
CURRENT FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: PCT US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1283
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-244-647-1283

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 907 ATTTCTTTGTGCTT 921
|||||

Db 15 ATTTCTTTGTGCTT 1

RESULT 945

US-10-293-338-2823/c
Sequence 2823, Application US/10293338
GENERAL INFORMATION:
APPLICANT: RosettaGenomics LTD
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
FILE REFERENCE: 45282
CURRENT APPLICATION NUMBER: US/10/293,338
CURRENT FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 8785
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2823
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
US-10-293-338-2823

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1245 CTCGACCCCATCCC 1259
|||||
Db 16 CTCGTCGCCCATCCC 2

RESULT 946

US-10-293-338-3206
Sequence 3206, Application US/10293338
GENERAL INFORMATION:
APPLICANT: RosettaGenomics LTD
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
FILE REFERENCE: 45282
CURRENT APPLICATION NUMBER: US/10/293,338
CURRENT FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 8785
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3206
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
US-10-293-338-3206

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1073 TCAGTCCCACTCCAG 1087
|||||
Db 2 TCAGTCCCACTCCGG 16

RESULT 947

US-10-303-778-6522
Sequence 6522, Application US/10303778
GENERAL INFORMATION:
APPLICANT: RosettaGenomics
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL
FILE REFERENCE: 47416
CURRENT APPLICATION NUMBER: US/10/303,778
CURRENT FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 17608
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6522
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens

US-10-303-778-6522

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 878 CAGGCACACAGTGC 892
| | | | |
Db 5 CAGGCACACAGTGC 19

RESULT 948

US-10-303-778-11820/c
; Sequence 11820, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11820
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-11820

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1253 CCATCCCCCAACCC 1267
| | | | |
Db 16 CCATCCCCCAACCC 2

RESULT 949

US-10-310-188-9763/c
; Sequence 9763, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9763
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-9763

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1253 CCATCCCCCAACCC 1267
| | | | |
Db 19 CCATCCCCCAACCC 5

RESULT 950

US-10-310-188-21659/c
; Sequence 21659, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487

; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21659
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-21659

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1253 CCATCCCCCAACCC 1267
| | | | |
Db 16 CCATCCCCCAACCC 2

RESULT 951

US-10-310-188-59914
; Sequence 59914, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59914
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-59914

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1092 CACCCCAACCTGGG 1106
| | | | |
Db 4 CACCCCAACCTGGG 18

RESULT 952

US-10-310-188-72707
; Sequence 72707, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72707
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-72707

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1192 GAGGTGGCACCACC 1206
| | | | |
Db 2 GAGGTGGCACCACC 16

```
RESULT 953
US-10-349-143-7262/c
; Sequence 7262, Application US/10349143
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET 020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7262
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19_bind
; OTHER INFORMATION: upstream amplification primer 99-3335 for SEQ 3328,
US-10-349-143-7262
Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 862 AAGGCACTGAGGAC 876
Db 16 AAGGCACTGAGAAC 2

RESULT 954
US-10-605-840-3515/c
; Sequence 3515, Application US/10605840
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VACCINIA REGULATORY
; FILE REFERENCE: 55027
; CURRENT APPLICATION NUMBER: US/10/605,840
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 3750
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3515
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-605-840-3515
Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 876 CTCAGGCACACAGT 890
Db 18 CTCAGGCTCCAGT 4

RESULT 955
US-10-707-147-1738
; Sequence 1738, Application US/10707147
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE REFERENCE: 49992
; CURRENT APPLICATION NUMBER: US/10/707,147
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 20189
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1738
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-707-147-1738
Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1050 GCCCTGCCCCAAA 1064
Db 1 GCCCTGCCCCAAA 15

RESULT 956
US-10-741-600-73310/c
; Sequence 73310, Application US/10741600
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73310
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-73310
Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 885 CACAGTGTGTGCC 899
Db 15 CACAGTGTGTGCC 1

RESULT 957
US-10-741-601-26190/c
; Sequence 26190, Application US/10741601
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26190
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-26190
Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 885 CACAGTGTGTGCC 899
Db 15 CACAGTGTGTGCC 1
```

```
RESULT 958
US-10-742-649-20/c
; Sequence 20, Application US/10742649
; GENERAL INFORMATION:
; APPLICANT: Beinfuhr, Claudia
; APPLICANT: Snaidr, Jiri
; TITLE OF INVENTION: METHOD FOR SPECIFIC FAST DETECTION OF
; TITLE OF INVENTION: RELEVANT BACTERIA IN DRINKING WATER
; FILE REFERENCE: MAIW4.006CL
; CURRENT APPLICATION NUMBER: US/10/742,649
; CURRENT FILING DATE: 2003-12-18
; PRIOR APPLICATION NUMBER: PCT/EP02/06809
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: DE 101 29 411.5
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: DE 101 60 666.4
; PRIOR FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-742-649-20

Query Match      0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1010 CACCTGAAAAAGAGG 1024
        |||||
Db       15 CACCGAAAAAGAGG 1

RESULT 959
US-60-082-614-1535/c
; Sequence 1535, Application US/60082614
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Chumakov, Ilya
; APPLICANT: Blumenfeld, Marta
; TITLE OF INVENTION: Biallelic markers for use in constructing a
; TITLE OF INVENTION: high density disequil
; NUMBER OF SEQUENCES: 2730
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/082,614
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: GENSET.020PR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 1535:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs

Query Match      0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1010 CACCTGAAAAAGAGG 1024
        |||||
Db       15 CACCGAAAAAGAGG 1

RESULT 958
US-10-742-649-20/c
; Sequence 20, Application US/10742649
; GENERAL INFORMATION:
; APPLICANT: Beinfuhr, Claudia
; APPLICANT: Snaidr, Jiri
; TITLE OF INVENTION: METHOD FOR SPECIFIC FAST DETECTION OF
; TITLE OF INVENTION: RELEVANT BACTERIA IN DRINKING WATER
; FILE REFERENCE: MAIW4.006CL
; CURRENT APPLICATION NUMBER: US/10/742,649
; CURRENT FILING DATE: 2003-12-18
; PRIOR APPLICATION NUMBER: PCT/EP02/06809
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: DE 101 29 411.5
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: DE 101 60 666.4
; PRIOR FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-742-649-20

Query Match      0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1010 CACCTGAAAAAGAGG 1024
        |||||
Db       15 CACCGAAAAAGAGG 1

RESULT 959
US-60-082-614-1535/c
; Sequence 1535, Application US/60082614
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Chumakov, Ilya
; APPLICANT: Blumenfeld, Marta
; TITLE OF INVENTION: Biallelic markers for use in constructing a
; TITLE OF INVENTION: high density disequil
; NUMBER OF SEQUENCES: 2730
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/082,614
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: GENSET.020PR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 1535:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs

Query Match      0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1416 GCTGGAGCTGCAGAA 1430
        |||||
Db       3 GGTGGAGCTGCAGAA 17

RESULT 960
US-10-317-277A-67/c
; Sequence 67, Application US/10317277A
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; TITLE OF INVENTION: Modulation of Estrogen-Responsive Finger Protein Expression
; FILE REFERENCE: RTS-0473
; CURRENT APPLICATION NUMBER: US/10/317,277A
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-317-277A-67

Query Match      0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1416 GCTGGAGCTGCAGAA 1430
        |||||
Db       18 GGTGGAGCTGCAGAA 4

RESULT 961
US-10-317-277A-142
; Sequence 142, Application US/10317277A
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; TITLE OF INVENTION: Modulation of Estrogen-Responsive Finger Protein Expression
; FILE REFERENCE: RTS-0473
; CURRENT APPLICATION NUMBER: US/10/317,277A
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 142
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-317-277A-142

Query Match      0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1416 GCTGGAGCTGCAGAA 1430
        |||||
Db       3 GGTGGAGCTGCAGAA 17
```

RESULT 962

PCT-US02-08937-165
; Sequence 165, Application PC/TUS0208937
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; TITLE OF INVENTION: LEINAMICIN BIOSYNTHESIS GENE CLUSTER AND ITS COMPONENTS AND THEIR
; FILE REFERENCE: 309T-000110PC
; CURRENT APPLICATION NUMBER: PCT/US02/08937
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/278,935
; PRIOR FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 165
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide PCR primer.
PCT-US02-08937-165

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 872 AGGACTCAGGACACACAG 889
| | | | | | | | | | | | | | | | | | | | | |
Db 1 ATGACCCAGGACACACTG 18

RESULT 963

PCT-US02-25943-29066/c
; Sequence 29066, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 29066
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (2810497)...(2810514)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectonObjectNumber = 31120
PCT-US02-25943-29066

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1119 GCCCAGTTCACCTTCAC 1136
| | | | | | | | | | | | | | | | | | | | | |
Db 18 GGCCAGTTCGCTTCAC 1

RESULT 964

PCT-US02-25943-51780
; Sequence 51780, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 51780
; LENGTH: 18

; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (5016571)...(5016588)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectonObjectNumber = 554
PCT-US02-25943-51780

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1120 CCCAGTTCACCTTCAC 1137
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CCCAGCTCCACCTAC 18

RESULT 965

PCT-US02-25943-60330/c
; Sequence 60330, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 60330
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (5873912)...(5873928)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectonObjectNumber = 646
PCT-US02-25943-60330

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1130 CCTCACCTCCAGCTCCA 1147
| | | | | | | | | | | | | | | | | | | | | |
Db 18 CCATCACCAGCAGCGCA 1

RESULT 966

PCT-US02-34679-341
; Sequence 341, Application PC/TUS0234679
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308PC
; CURRENT APPLICATION NUMBER: PCT/US02/34679
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09

PRIOR APPLICATION NUMBER: US 60/337,052
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: US 60/368,919
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 564
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 341
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
PCT-US02-34679-343

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1116 CGTGCCAGTCCACCTT 1133
||| ||||| |||||
Db 1 CGAGCCAGATCAACCTT 18

RESULT 967
PCT-US02-34679-343
Sequence 343, Application PC/TUS0234679
GENERAL INFORMATION:
APPLICANT: Becker, Kenneth David
APPLICANT: Velicelebi, Gonul
APPLICANT: Elliot, Kathryn J.

APPLICANT: Wang, Xin
APPLICANT: Tanzi, Rudolph E.
APPLICANT: Bertram, Lars
APPLICANT: Saunders, Aleister J.
APPLICANT: Mullin, Kristina M.
APPLICANT: Sampson, Andrew Johnson
APPLICANT: Blacker, Deborah Lynne
TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
FILE REFERENCE: 37481-3308PC
CURRENT APPLICATION NUMBER: PCT/US02/34679
CURRENT FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: US 60/339,525
PRIOR FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 60/338,010
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/336,929
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/338,363
PRIOR FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: US 60/337,052
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: US 60/368,919
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 564
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 343
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
PCT-US02-34679-343

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1116 CGTGCCAGTCCACCTT 1133
||| ||||| |||||
Db 1 CGAGCCAGATCAACCTT 18

RESULT 968
PCT-US98-17838-74
Sequence 74, Application PC/TUS9817838
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Splawski, Igor
TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH
TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
FILE REFERENCE: 2323-131
CURRENT APPLICATION NUMBER: PCT/US98/17838
CURRENT FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: 08/921,066
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 08/739,383
EARLIER FILING DATE: 1996-10-29
EARLIER APPLICATION NUMBER: 60/019,014
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 60/094,477
EARLIER FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 74
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US98-17838-74

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1253 CCATCCCCAACCCCTTC 1270
||| ||||| |||||
Db 1 CCATCCCCAGCCCATC 18

RESULT 969
PCT-US99-08268-26/c
Sequence 26, Application PC/TUS9908268
GENERAL INFORMATION:
APPLICANT: ISIS Pharmaceuticals, Inc.
APPLICANT: Cowser, Lex M.
APPLICANT: Baker, Brenda F.
APPLICANT: McNeil, John
APPLICANT: Sasmor, Susan M.
APPLICANT: Freier, Henri M.
APPLICANT: Brooks, Douglas G.
APPLICANT: Ohashi, Cara
APPLICANT: Wyatt, Jacqueline R.
APPLICANT: Borchers, Alexander
APPLICANT: Vickers, Timothy A.
TITLE OF INVENTION: Identification of Genetic Targets for Modulation by
TITLE OF INVENTION: Oligonucleotides and Generation of Oligonucleotides for Gene
FILE REFERENCE: ISIS-3456
CURRENT APPLICATION NUMBER: PCT/US99/08268
CURRENT FILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: US 09/067,638
EARLIER FILING DATE: 1998-04-28
EARLIER APPLICATION NUMBER: US 60/081,483
EARLIER FILING DATE: 1998-04-13
NUMBER OF SEQ ID NOS: 372
SEQ ID NO 26
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
PCT-US99-08268-26

```
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1006 TCGACACCTGAAAGAG 1023
Db 18 TAGACACCTGGAACAG 1

RESULT 970
PCT-US99-08268-221/c
; Sequence 221, Application PC/TUS9908268
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc.
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasnor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: Identification of Genetic Targets for Modulation by
; TITLE OF INVENTION: Oligonucleotides and Generation of Oligonucleotides for Gene
; TITLE OF INVENTION: Modulation
; FILE REFERENCE: ISIS-3456
; CURRENT APPLICATION NUMBER: PCT/US99/08268
; CURRENT FILING DATE: 1999-04-13
; EARLIER APPLICATION NUMBER: US 09/067,638
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: US 60/081,483
; EARLIER FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 372
; SEQ ID NO 221
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US99-08268-221

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1120 CCCAGTCCACCTCACC 1137
Db 18 CTCATTCCACCTCACC 1

RESULT 971
PCT-US99-08765A-26/c
; Sequence 26, Application PC/TUS9908765A
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett and Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF
; TITLE OF INVENTION: CD40 EXPRESSION
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
```

```
; APPLICATION NUMBER: PCT/US99/08765A
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/071,433
; FILING DATE: March 12, 1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0355
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 810-1515
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US99-08765A-26

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1006 TCGACACCTGAAAGAG 1023
Db 18 TAGACACCTGGAACAG 1

RESULT 972
PCT-US99-10260-74
; Sequence 74, Application PC/TUS9910260
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KvLQT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: PCT/US99/10260
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US99-10260-74

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1253 CCATCCCCAACCCCTTC 1270
Db 1 CCATCCCCAGCCCCATC 18

RESULT 973
US-08-489-967-1
; Sequence 1, Application US/08489967
```


TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-067-638B-26

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1006 TCGACACCTGAAAAAGAG 1023
| | | | | | | | | | | | | | | | | |
Db 18 TAGACACCTGGACACAG 1

RESULT 976

US-09-135-021-72
Sequence 72, Application US/09135021
GENERAL INFORMATION:
APPLICANT: Splawski, Igor
TITLE OF INVENTION: A HOMOLOGOUS MUTATION IN KVLQ1 WHICH CAUSES JERVELL
FILE REFERENCE: 2323-128
CURRENT APPLICATION NUMBER: US/09/135,021
EARLIER FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/874,655
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/094,477
EARLIER FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 72
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-09-135-021-72

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1253 CCATCCCCAACCCCTTC 1270
| | | | | | | | | | | | | | | | | |
Db 1 CCATCCCCACGCCCATC 18

RESULT 977

US-09-295-463-26/c
Sequence 26, Application US/09295463
GENERAL INFORMATION:
APPLICANT: Cowser, Lex M.
APPLICANT: Baker, Brenda F.
APPLICANT: McNeil, John
APPLICANT: Freier, Susan M.
APPLICANT: Sasmor, Henri M.
APPLICANT: Brooks, Douglas G.
APPLICANT: Ohashi, Cara
APPLICANT: Wyatt, Jacqueline R.
APPLICANT: Borchers, Alexander
APPLICANT: Vickers, Timothy A.
TITLE OF INVENTION: Identification of Genetic Targets for Modulation by
TITLE OF INVENTION: Oligonucleotides and Generation of Oligonucleotides for Gene
FILE REFERENCE: ISIS-3455
CURRENT APPLICATION NUMBER: US/09/295,463
CURRENT FILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: US/09/067,638

EARLIER FILING DATE: 1998-04-28
EARLIER APPLICATION NUMBER: US 60/081,483
EARLIER FILING DATE: 1998-04-13
NUMBER OF SEQ ID NOS: 372
SEQ ID NO 26
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-295-463-26

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1006 TCGACACCTGAAAAAGAG 1023
| | | | | | | | | | | | | | | | | |
Db 18 TAGACACCTGGACACAG 1

RESULT 978

US-09-295-463-221/c
Sequence 221, Application US/09295463
GENERAL INFORMATION:
APPLICANT: Cowser, Lex M.
APPLICANT: Baker, Brenda F.
APPLICANT: McNeil, John
APPLICANT: Freier, Susan M.
APPLICANT: Sasmor, Henri M.
APPLICANT: Brooks, Douglas G.
APPLICANT: Ohashi, Cara
APPLICANT: Wyatt, Jacqueline R.
APPLICANT: Borchers, Alexander
APPLICANT: Vickers, Timothy A.
TITLE OF INVENTION: Identification of Genetic Targets for Modulation by
TITLE OF INVENTION: Oligonucleotides and Generation of Oligonucleotides for Gene
FILE REFERENCE: ISIS-3455
CURRENT APPLICATION NUMBER: US/09/295,463
CURRENT FILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: US 09/067,638
EARLIER FILING DATE: 1998-04-28
EARLIER APPLICATION NUMBER: US 60/081,483
EARLIER FILING DATE: 1998-04-13
NUMBER OF SEQ ID NOS: 372
SEQ ID NO 221
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-295-463-221

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1120 CCCAGTTCACCTTCACC 1137
| | | | | | | | | | | | | | | | | |
Db 18 CTCTATTCACCTTCACC 1

RESULT 979

US-09-541-946-1083
Sequence 1083, Application US/09541946
GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Cargill, Michele
APPLICANT: Altschuler, David M.
APPLICANT: Ireland, James S.
APPLICANT: Sklar, Pamela
APPLICANT: Patil, Nila


```
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Daley, George Q.
; TITLE OF INVENTION: CHARACTERIZATION OF SINGLE NUCLEOTIDE
; FILE REFERENCE: 2825.1017-003
; CURRENT APPLICATION NUMBER: US/09/541,946
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,248
; NUMBER OF SEQ ID NOS: 2889
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1083
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-541-946-1083
```

```
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1197 GGCACCACTATCAGG 1214
||| ||||| |||||
Db 1 GGCATCACCTCTCTGGG 18
```

```
RESULT 980
US-09-541-946-1090
; Sequence 1090, Application US/09541946
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Altshuler, David M.
; APPLICANT: Ireland, James S.
; APPLICANT: Sklar, Pamela
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Daley, George Q.
; TITLE OF INVENTION: CHARACTERIZATION OF SINGLE NUCLEOTIDE
; FILE REFERENCE: 2825.1017-003
; CURRENT APPLICATION NUMBER: US/09/541,946
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,248
; NUMBER OF SEQ ID NOS: 2889
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1090
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-541-946-1090
```

```
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1197 GGCACCACTATCAGG 1214
||| ||||| |||||
Db 1 GGCATCACCTCTCTGGG 18
```

```
RESULT 981
US-09-541-946-1101
; Sequence 1101, Application US/09541946
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Altshuler, David M.
```

```
; APPLICANT: Ireland, James S.
; APPLICANT: Sklar, Pamela
; APPLICANT: Patil, Nila
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Daley, George Q.
; TITLE OF INVENTION: CHARACTERIZATION OF SINGLE NUCLEOTIDE
; FILE REFERENCE: 2825.1017-003
; CURRENT APPLICATION NUMBER: US/09/541,946
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,248
; NUMBER OF SEQ ID NOS: 2889
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1101
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-541-946-1101
```

```
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1197 GGCACCACTATCAGG 1214
||| ||||| |||||
Db 1 GGCATCACCTCTCTGGG 18
```

```
RESULT 982
US-09-582-533A-251
; Sequence 251, Application US/09582533A
; GENERAL INFORMATION:
; APPLICANT: VIDER
; TITLE OF INVENTION: METHOD OR IDENTIFYING AND CHARACTERIZING CELLS AND TISSUES
; FILE REFERENCE: 24296
; CURRENT APPLICATION NUMBER: US/09/582,533A
; CURRENT FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 251
; LENGTH: 18
; TYPE: DNA
; ORGANISM: human
US-09-582-533A-251
```

```
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1093 ACCCCACCTGGGCTTC 1110
||| ||||| |||||
Db 1 AGCCCAAGCTGGGTTTC 18
```

```
RESULT 983
US-09-868-301-24/c
; Sequence 24, Application US/09868301
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF ELK-1 EXPRESSION
; FILE REFERENCE: RTSP-0127
; CURRENT APPLICATION NUMBER: US/09/868,301
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 24
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

; OTHER INFORMATION: Synthetic
US-09-868-301-24

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1120 CCAGTTCACCTTCACC 1137
Db 18 CTCTATTCACCTTCACC 1

RESULT 984

US-09-868-301A-24/c
; Sequence 24, Application US/09868301A
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF ELK-1 EXPRESSION
; FILE REFERENCE: RTSP-0127
; CURRENT APPLICATION NUMBER: US/09/868,301A
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 24
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-868-301A-24

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1120 CCAGTTCACCTTCACC 1137
Db 18 CTCTATTCACCTTCACC 1

RESULT 985

US-10-116-325-26/c
; Sequence 26, Application US/10116325
; GENERAL INFORMATION:
; APPLICANT: Cowser, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Samor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: Identification of Genetic Targets For Modulation By Oligonucleotides
; FILE REFERENCE: ISIS026
; CURRENT APPLICATION NUMBER: US/10/116,325
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/067,638
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/081,483
; PRIOR FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Novel Sequence
US-10-116-325-26

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1006 TCGACACCTGAAAAGAG 1023
Db 18 TAGACACCTGGACAGAG 1

RESULT 986

US-10-138-316-74
; Sequence 74, Application US/10138316
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; TITLE OF INVENTION: KCNE1 AS AN LQT GENE
; FILE REFERENCE: 2323-162
; CURRENT APPLICATION NUMBER: US/10/138,316
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/444,295
; PRIOR FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: 09/135,020
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-138-316-74

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1253 CCATCCCCAACCCCTTC 1270
Db 1 CCATCCCCAGCCCATC 18

RESULT 987

US-10-227-565-29066/c
; Sequence 29066, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 29066
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (2810497)...(2810514)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 311
US-10-227-565-29066

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1119 GCCAGTTCACCTTCAC 1136
 Db 18 GCCAGTTCGTCCTTCAC 1

RESULT 988

US-10-227-565-51780
 ; Sequence 51780, Application US/10227565
 ; GENERAL INFORMATION:
 ; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
 ; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
 ; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
 ; CURRENT APPLICATION NUMBER: US/10/227,565
 ; CURRENT FILING DATE: 2002-08-26
 ; NUMBER OF SEQ ID NOS: 64158
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 51780
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
 ; FEATURE:
 ; LOCATION: (5016571)....(5016588)
 ; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 55445
 US-10-227-565-51780

Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 6.1e+02;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1120 CCCAGTTCACCTTCACC 1137
 Db 1 CCCAGTTCGACATCACC 18

RESULT 989

US-10-227-565-60330/c
 ; Sequence 60330, Application US/10227565
 ; GENERAL INFORMATION:
 ; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
 ; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
 ; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
 ; CURRENT APPLICATION NUMBER: US/10/227,565
 ; CURRENT FILING DATE: 2002-08-26
 ; NUMBER OF SEQ ID NOS: 64158
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 60330
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
 ; FEATURE:
 ; LOCATION: (5873912)....(5873928)
 ; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 64604
 US-10-227-565-60330

Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 6.1e+02;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1130 CCTTCACCTCGAGTCACA 1147
 Db 18 CCATCAGGCGAGCGCA 1

RESULT 990

US-10-266-090-38112/c
 ; Sequence 38112, Application US/10266090
 ; GENERAL INFORMATION:
 ; APPLICANT: GOFF, STEPHEN
 ; APPLICANT: BONAN, CAROLINE
 ; APPLICANT: COLBERT, MICHELLE
 ; APPLICANT: WANG, RONG-LIN

; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
 ; TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES

; FILE REFERENCE: NADII.058C1
 ; CURRENT APPLICATION NUMBER: US/10/266,090
 ; CURRENT FILING DATE: 2002-10-03
 ; PRIOR APPLICATION NUMBER: US 10/260,703
 ; PRIOR FILING DATE: 2002-09-26
 ; PRIOR APPLICATION NUMBER: US 60/326,117
 ; PRIOR FILING DATE: 2001-09-26
 ; NUMBER OF SEQ ID NOS: 51812
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 38112
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
 US-10-266-090-38112

Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 6.1e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1249 GACCCCATCCCAACCCC 1266
 Db 18 GACCACTCTCCCAACCCC 1

RESULT 991

US-10-266-090-40503
 ; Sequence 40503, Application US/10266090
 ; GENERAL INFORMATION:
 ; APPLICANT: GOFF, STEPHEN
 ; APPLICANT: BONAN, CAROLINE
 ; APPLICANT: COLBERT, MICHELLE
 ; APPLICANT: WANG, RONG-LIN
 ; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
 ; FILE REFERENCE: NADII.058C1
 ; CURRENT APPLICATION NUMBER: US/10/266,090
 ; CURRENT FILING DATE: 2002-10-03
 ; PRIOR APPLICATION NUMBER: US 10/260,703
 ; PRIOR FILING DATE: 2002-09-26
 ; PRIOR APPLICATION NUMBER: US 60/326,117
 ; PRIOR FILING DATE: 2001-09-26
 ; NUMBER OF SEQ ID NOS: 51812
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 40503
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
 US-10-266-090-40503

Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 6.1e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1122 CAGTTCACCTTCACCTC 1139
 Db 1 CAGTCCACCAACCACTC 18

RESULT 992

US-10-266-090-47008
 ; Sequence 47008, Application US/10266090
 ; GENERAL INFORMATION:
 ; APPLICANT: GOFF, STEPHEN
 ; APPLICANT: BONAN, CAROLINE
 ; APPLICANT: COLBERT, MICHELLE
 ; APPLICANT: WANG, RONG-LIN
 ; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE

```
; TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
; FILE REFERENCE: NADII.058C1
; CURRENT APPLICATION NUMBER: US/10/266,090
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 10/260,703
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/326,117
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 51812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47008
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-47008
```

```
Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1129 ACCTTCACCTCCAGCTCC 1146
|||||
DB 1 ACCTCCACCTCTCTCTCC 18
```

```
RESULT 993
US-10-266-090-51552
; Sequence 51552, Application US/10266090
; GENERAL INFORMATION:
; APPLICANT: GOFF, STEPHEN
; APPLICANT: BONAN, CAROLINE
; APPLICANT: COLBERT, MICHELLE
; APPLICANT: WANG, RONG-LIN
; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
; TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
; FILE REFERENCE: NADII.058C1
; CURRENT APPLICATION NUMBER: US/10/266,090
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 10/260,703
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/326,117
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 51812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51552
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-51552
```

```
Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1128 CACCTTCACCTCCAGCTC 1145
|||||
DB 1 CACCAGCTCTCTCTCTCC 18
```

```
RESULT 994
US-10-266-090-51728
; Sequence 51728, Application US/10266090
; GENERAL INFORMATION:
; APPLICANT: GOFF, STEPHEN
; APPLICANT: BONAN, CAROLINE
; APPLICANT: COLBERT, MICHELLE
; APPLICANT: WANG, RONG-LIN
; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
; TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
```

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; FILE REFERENCE: NADII.058C1
; CURRENT APPLICATION NUMBER: US/10/266,090
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 10/260,703
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/326,117
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 51812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51728
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-51728
```

```
Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY 1129 ACCTTCACCTCCAGCTCC 1146
|||||
DB 1 ACCTCCACCTCTCTCTCC 18
```

```
RESULT 995
US-10-282-174-341
; Sequence 341, Application US/10282174
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Elliott, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308
; CURRENT APPLICATION NUMBER: US/10/282,174
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 341
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-282-174-341
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Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1116 CGTGCCCGAGTTCACCTT 1133
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Db 1 CGAGCCAGATCAACTT 18
|| ||||| || |||||

RESULT 996
US-10-282-174-343
; Sequence 343, Application US/10282174
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Vellicelebi, Gonul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308
; CURRENT APPLICATION NUMBER: US/10/282,174
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-282-174-343

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1116 CGTCCAGTTCACCTT 1133
|| ||||| || |||||

Db 1 CGAGCCAGATCAACTT 18
|| ||||| || |||||

RESULT 997
US-10-293-338-2066
; Sequence 2066, Application US/10293338
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 45282
; CURRENT APPLICATION NUMBER: US/10/293,338
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 8785
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2066
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-338-2066

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1251 CCCATCCCAACCCCT 1268
|| ||||| || |||||

Db 1 CCCCTCCCAACCCCT 18
|| ||||| || |||||

RESULT 998
US-10-293-338-6601
; Sequence 6601, Application US/10293338
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 45282
; CURRENT APPLICATION NUMBER: US/10/293,338
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 8785
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6601
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-338-6601

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 889 GTGCTGTTCACCTGGC 906
|| ||||| || |||||

Db 1 GTGCTGTTCACCTGGC 18
|| ||||| || |||||

RESULT 999
US-10-303-778-3233
; Sequence 3233, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL
; TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3233
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-3233

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 909 TTTCTTTGGCTTTGCT 926
|| ||||| || |||||

Db 1 TTTCTTTGGCTTTGCT 18
|| ||||| || |||||

RESULT 1000
US-10-303-778-4618/c
; Sequence 4618, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL
; TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26

; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4618
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-4618

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1248 CGACCCCATCCCAACCC 1265
| | | | | | | | | | | | | | | | | |
Db 18 CCACCCCAACCCCAACCC 1

RESULT 1001
US-10-303-778-4666/c
; Sequence 4666, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4666
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-4666

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1248 CGACCCCATCCCAACCC 1265
| | | | | | | | | | | | | | | | | |
Db 18 CCACCCCAACCCCAACCC 1

RESULT 1002
US-10-303-778-4999/c
; Sequence 4999, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4999
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-4999

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1128 CACCTTCACCTCCAGCTC 1145
| | | | | | | | | | | | | | | | | |
Db 18 CACCCCAACCCCAACCTC 1

RESULT 1003
US-10-303-778-8192/c

; Sequence 8192, Application US/10303778
; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8192
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-8192

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1119 GCCCAGTTCACCTTCAC 1136
| | | | | | | | | | | | | | | | | |
Db 18 GCCCAGTTCACCTTCAC 1

RESULT 1004
US-10-310-188-4288/c
; Sequence 4288, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4288
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-4288

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 908 TTTTCITTTGGCTTTGGC 925
| | | | | | | | | | | | | | | | | |
Db 18 TTTTCITTTGGCTTTGGC 1

RESULT 1005
US-10-310-188-5478
; Sequence 5478, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5478
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-5478

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 909 TTCTTTGGCTCTTGCT 926
Db 1 TTCTTTGGCATTCCT 18

RESULT 1006
US-10-310-188-6210
; Sequence 6210, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6210
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-6210

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1243 GCTCGACCCCATCCCC 1260
Db 1 GCTCAGCCCTTCCTCC 18

RESULT 1007
US-10-310-188-9659/c
; Sequence 9659, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9659
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-9659

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1248 CGACCCCATCCCCAACCC 1265
Db 1 CCACCCCATCCCCAACCC 1

RESULT 1008
US-10-310-188-9706/c
; Sequence 9706, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9706

; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-9706

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1248 CGACCCCATCCCCAACCC 1265
Db 1 CCACCCCATCCCCAACCC 1

RESULT 1009
US-10-310-188-10527/c
; Sequence 10527, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10527
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-10527

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1128 CACCTTCACCTCCAGCTC 1145
Db 18 CACCCCATCCCCAGCTC 1

RESULT 1010
US-10-310-188-11033
; Sequence 11033, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11033
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-11033

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1235 CAGCCCTCGCTCCGACC 1252
Db 1 CGCCCGCGCTCCGCCC 18

RESULT 1011
US-10-310-188-17069
; Sequence 17069, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics

```
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17069
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-17069

Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1223 CCATCCTTGGCAGAGCCC 1240
||||| |||||||
Db 1 CCGTCGGTGGCAGAGCCC 18

RESULT 1012
US-10-310-188-26440
; Sequence 26440, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26440
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-26440

Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1230 TGCAGACGCTCGCCCTC 1247
||||| |||||||
Db 1 TGCAGACGCTCGCCAC 18

RESULT 1013
US-10-310-188-42111/c
; Sequence 42111, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42111
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-42111

Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1247 CCGACCCCATCCCAACC 1264
||||| ||||||| ||
```

```
Db 18 CCGCCCCCATCCCGCCC 1

RESULT 1014
US-10-310-188-42218/c
; Sequence 42218, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42218
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-42218

Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1139 CCAGCTCCACCTATACCC 1156
||||| |||||||
Db 18 CCAGCCCGAGCTCTACCC 1

RESULT 1015
US-10-310-188-51868/c
; Sequence 51868, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51868
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-51868

Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1244 CCTCCGACCCCATCCCA 1261
||||| |||||||
Db 18 CCTCCGACCCCATCCCA 1

RESULT 1016
US-10-310-188-58107/c
; Sequence 58107, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58107
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
```


US-10-310-188-58107

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 913 TTGTGCTTTGCTTTTA 930
DB 18 TTCTCTTTGCTTTCTTA 1

RESULT 1017

US-10-310-188-64553
; Sequence 64553, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64553
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-64553

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1242 CGCTCCGACCCCTCC 1259
DB 1 CCGCTCTACCCCTCC 18

RESULT 1018

US-10-310-188-64750
; Sequence 64750, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64750
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-64750

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1581 CGGCCCCGCGCCCTCC 1598
DB 1 CGCCCCGCGCCCTCC 18

RESULT 1019

US-10-310-188-69028/c
; Sequence 69028, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487

; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69028
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-69028

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1254 CATCCCAACCCCTTCA 1271
DB 18 CATCCCTGCCCATTC A 1

RESULT 1020

US-10-310-188-71360/c
; Sequence 71360, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71360
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-71360

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 909 TTCTTTGCTTTGCTT 926
DB 18 TTCTTTGCTTTGCTT 1

RESULT 1021

US-10-310-188-72865/c
; Sequence 72865, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72865
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-72865

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1252 CCCATCCCAACCCCTT 1269
DB 18 CCCACCCCAACCCCTT 1

RESULT 1022

US-10-310-188-75117/c
; Sequence 75117, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75117
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-75117

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1242 CGCCTCCGACCCGATCCC 1259
Db 18 CGCCCGACCCGATCCC 1

RESULT 1023

US-10-310-188-77971/c
; Sequence 77971, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77971
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-77971

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 743 ACACCGTGGCAGCTGCC 760
Db 18 ACCCGTGGCAGCTGCC 1

RESULT 1024

US-10-310-188-80411
; Sequence 80411, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80411
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-80411

Query Match 0.6%; Score 13.2; DB 1; Length 18;

Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 870 TGAGGACTCAGGCACCCAC 887
Db 1 TGGGACTCAGGCACCCAC 18

RESULT 1025

US-10-310-188-85848
; Sequence 85848, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85848
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-85848

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 869 CTGAGGACTCAGGCACCA 886
Db 1 CAGAGGAGCAGGCACCA 18

RESULT 1026

US-10-310-188-85920/c
; Sequence 85920, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85920
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-85920

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 927 TTATCCCTCCTCTTCAT 944
Db 18 TTCATCCCTCCTCTTCCT 1

RESULT 1027

US-10-310-188-86807/c
; Sequence 86807, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86807
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-86807
```

```
Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1211 AGGGGGCTGACCCCATCC 1228
      ||||| ||||| |||||
Db 18 AGGGGCTGAGCCATCC 1
```

```
RESULT 1028
US-10-314-657-165
; Sequence 165, Application US/10314657
; GENERAL INFORMATION:
; APPLICANT: SHEN, Ben
; APPLICANT: CHENG, Yi-Qiang
; APPLICANT: TANG, Gong-Li
; TITLE OF INVENTION: Discrete Acyltransferases Associated with Type I Polyketide
; FILE REFERENCE: 054030-0021
; CURRENT APPLICATION NUMBER: US/10/314,657
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: PCT/US02/08937
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/278,935
; PRIOR FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 165
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Streptomyces atroolivaceus
US-10-314-657-165
```

```
Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 872 AGGACTCAGGCACACAG 889
      ||||| ||||| |||||
Db 1 ATGACCCAGGCACACTG 18
```

```
RESULT 1029
US-10-349-143-4110/c
; Sequence 4110, Application US/10349143
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4110
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
```

```
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-13332 for SEQ 176,
US-10-349-143-4110
```

```
Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 813 GAAAAGCCTGAGTGCAC 830
      ||||| ||||| |||||
Db 18 GAAAAGCCTCACTGCAC 1
```

```
RESULT 1030
US-10-349-143-4877/c
; Sequence 4877, Application US/10349143
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4877
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-18386 for SEQ 943,
US-10-349-143-4877
```

```
Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1130 CCTTCACCTCCAGTCCA 1147
      ||||| ||||| |||||
Db 18 CTTTTACCTCCACTCCA 1
```

```
RESULT 1031
US-10-367-832A-29066/c
; Sequence 29066, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 29066
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (2810497)...(2810514)
; OTHER INFORMATION: Chromosome = 1 Strand = positive
US-10-367-832A-29066
```

```

Query Match
Best Local Similarity 0.6%; Score 13.2; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1119 GCCCAGTTCACCTTCAC 1136
DB 18 GCCCAGTTCGCTTCAC 1

RESULT 1032
US-10-367-832A-51780
; Sequence 51780, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 51780
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (5016571)...(5016588)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 55445
US-10-367-832A-51780

Query Match
Best Local Similarity 0.6%; Score 13.2; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1120 CCCAGTCCACCTTCACC 1137
DB 1 CCCAGTCCGACCATCACC 18

RESULT 1033
US-10-367-832A-60330/c
; Sequence 60330, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 60330
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (5873912)...(5873928)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 64604
US-10-367-832A-60330

Query Match
Best Local Similarity 0.6%; Score 13.2; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1130 CCTTCACCTCCAGCTCCA 1147
DB 18 CCATCACCAGCGGCA 1

RESULT 1034
US-10-368-643-74
; Sequence 74, Application US/10368643
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.

```

```

; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-163
; CURRENT APPLICATION NUMBER: US/10/368,643
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/597,731
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: US 09/135,010
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: US 60/094,477
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: US 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: US 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: US 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-368-643-74

Query Match
Best Local Similarity 0.6%; Score 13.2; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1253 CCATCCCCACCCGCTTC 1270
DB 1 CCATCCCCAGCCCCATC 18

RESULT 1035
US-10-388-263-26/c
; Sequence 26, Application US/10388263
; GENERAL INFORMATION:
; APPLICANT: Cowsett, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasmor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-26

Query Match
Best Local Similarity 0.6%; Score 13.2; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 1006 TCGACACCTGAAAAGAG 1023
Db 18 TAGACACCTGGACAG 1

RESULT 1036

US-10-388-263-221/c
; Sequence 221, Application US/10388263
; GENERAL INFORMATION:
; APPLICANT: Cowsett, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasmor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 221
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-221

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1120 CCCAGTTCACCTTCACC 1137
Db 18 CTCATTCACCTTCACC 1

RESULT 1037

US-10-423-007-31/c
; Sequence 31, Application US/10423007
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; APPLICANT: KOISHIHARA, YASUO
; APPLICANT: KOSAKA, MASAOKI
; TITLE OF INVENTION: GENOMIC GENE ENCODING HM 1.24 ANTIGEN PROTEIN AND
; TITLE OF INVENTION: PROMOTER THEREOF
; FILE REFERENCE: 053466/0285
; CURRENT APPLICATION NUMBER: US/10/423,007
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US/09/622,166A
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: PCT/JF99/00884
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: 10-60617
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 10-93883
; PRIOR FILING DATE: 1998-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 31
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer

US-10-423-007-31

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1020 AGAGGGGAGCTTGAGG 1037
Db 18 AGTGGAGGAGCTTGAGG 1

RESULT 1038

US-10-600-009-341
; Sequence 341, Application US/10600009
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Eliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308B
; CURRENT APPLICATION NUMBER: US/10/600,009
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/282,174
; PRIOR FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 341
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-600-009-341

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1116 CGTCCCGAGTTCCACCTT 1133
Db 1 CGAGCCGAGATCAACCTT 18

RESULT 1039

US-10-600-009-343
; Sequence 343, Application US/10600009
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Eliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.

; APPLICANT: Bertram, Lars
 ; APPLICANT: Saunders, Aleister J.
 ; APPLICANT: Mullin, Kristina M.
 ; APPLICANT: Sampson, Andrew Johnson
 ; APPLICANT: Blacker, Deborah Lynne
 ; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
 ; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
 ; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
 ; FILE REFERENCE: 37481-3308B
 ; CURRENT APPLICATION NUMBER: US/10/600,009
 ; CURRENT FILING DATE: 2003-08-18
 ; PRIOR APPLICATION NUMBER: US 60/339,525
 ; PRIOR FILING DATE: 2001-10-25
 ; PRIOR APPLICATION NUMBER: US 60/338,010
 ; PRIOR FILING DATE: 2001-11-08
 ; PRIOR APPLICATION NUMBER: US 60/336,929
 ; PRIOR FILING DATE: 2001-11-08
 ; PRIOR APPLICATION NUMBER: US 60/338,363
 ; PRIOR FILING DATE: 2001-11-09
 ; PRIOR APPLICATION NUMBER: US 60/337,052
 ; PRIOR FILING DATE: 2001-12-04
 ; PRIOR APPLICATION NUMBER: US 60/368,919
 ; PRIOR FILING DATE: 2002-03-28
 ; PRIOR APPLICATION NUMBER: US 10/282,174
 ; PRIOR FILING DATE: 2002-10-25
 ; NUMBER OF SEQ ID NOS: 564
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 343
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Primer
 US-10-600-009-343

Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 6.1e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1116 CGTCCAGTTCACCTT 1133
 DB 1 CGAGCCAGATCAACCTT 18

RESULT 1040
 US-60-216-745-8632
 ; Sequence 8632, Application US/60216745
 ; GENERAL INFORMATION:
 ; APPLICANT: Cohen, Daniel
 ; APPLICANT: Blumenfeld, Marta
 ; APPLICANT: Chumakov, Ilya
 ; APPLICANT: Abderrahim, Hadi
 ; APPLICANT: Dufaire-Gare, Isabelle
 ; TITLE OF INVENTION: BIALLELIC MARKER MAPS FOR USE IN CONSTRUCTING A HIGH DENSITY...
 ; FILE REFERENCE: 84.Usi.PRO
 ; CURRENT APPLICATION NUMBER: US/60/216,745
 ; CURRENT FILING DATE: 2000-06-30
 ; NUMBER OF SEQ ID NOS: 13665
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 8632
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; NAME/KEY: primer_bind
 ; LOCATION: 1..18
 ; OTHER INFORMATION: upstream amplification primer 99-31024 for SEQ 4101,
 US-60-216-745-8632

Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 6.1e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1020 AGAGGGGAGCTTGAGG 1037
 DB 1 AGAGGAGGAGTTGATGG 18
 RESULT 1041
 US-09-949-427-355/c
 ; Sequence 355, Application US/09949427
 ; GENERAL INFORMATION:
 ; APPLICANT: Bodnar, Jackie S.
 ; APPLICANT: Castellani, Lawrence W.
 ; APPLICANT: Chatterjee, Aurobindo
 ; APPLICANT: de Jong, Pieter
 ; APPLICANT: Luisis, Aldons J.
 ; APPLICANT: Ohmen, Jeff
 ; APPLICANT: Ross, David
 ; APPLICANT: Tafuri, Sherrie
 ; APPLICANT: Wu, Chenyan
 ; TITLE OF INVENTION: Gene and Sequence Variation Associated with Cancer
 ; FILE REFERENCE: 02810.0014.NPUS02
 ; CURRENT APPLICATION NUMBER: US/09/949,427
 ; CURRENT FILING DATE: 2001-09-07
 ; PRIOR APPLICATION NUMBER: 60/231,322
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 405
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 355
 ; LENGTH: 21
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Primer
 US-09-949-427-355

Query Match 0.6%; Score 13.2; DB 1; Length 21;
 Best Local Similarity 83.3%; Pred. No. 7e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 36 GGAGCCTCAGTCCAGAGA 53
 DB 20 GGAGCCTCAGTCCCTCAGA 3

RESULT 1042
 US-09-949-427A-355/c
 ; Sequence 355, Application US/09949427A
 ; GENERAL INFORMATION:
 ; APPLICANT: Bodnar, Jackie S.
 ; APPLICANT: Castellani, Lawrence W.
 ; APPLICANT: Chatterjee, Aurobindo
 ; APPLICANT: de Jong, Pieter
 ; APPLICANT: Luisis, Aldons J.
 ; APPLICANT: Ohmen, Jeff
 ; APPLICANT: Ross, David
 ; APPLICANT: Tafuri, Sherrie
 ; APPLICANT: Wu, Chenyan
 ; TITLE OF INVENTION: Gene and Sequence Variation Associated with Cancer
 ; FILE REFERENCE: 8038 02810-0014
 ; CURRENT APPLICATION NUMBER: US/09/949,427A
 ; CURRENT FILING DATE: 2001-09-07
 ; PRIOR APPLICATION NUMBER: 60/231,322
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 415
 ; SOFTWARE: PatentIn version 2.1
 ; SEQ ID NO 355
 ; LENGTH: 21
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Primer
 US-09-949-427A-355

Query Match 0.6%; Score 13.2; DB 1; Length 21;

```
Best Local Similarity 83.3%; Pred. No. 7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 36 GGAGCCTCAGTCACAGAGA 53
DB 20 GGAGCCTCAGTCCTCAGA 3

RESULT 1043
US-09-949-428-355/c
; Sequence 355, Application US/09949428
; GENERAL INFORMATION:
; APPLICANT: Bodnar, Jackie S.
; APPLICANT: Castellani, Lawrence W.
; APPLICANT: Chatterjee, Aurobindo
; APPLICANT: de Jong, Pieter
; APPLICANT: Lusi, Aldons J.
; APPLICANT: Ohmen, Jeff
; APPLICANT: Ross, David
; APPLICANT: Tafuri, Sherrie
; APPLICANT: Wu, Chenyan
; TITLE OF INVENTION: Gene and Sequence Variation Associated with Lipid Disorder
; FILE REFERENCE: 02810.0014.NPUS01
; CURRENT APPLICATION NUMBER: US/09/949,428
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/231,322
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 355
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-949-428-355

Query Match 0.6%; Score 13.2; DB 1; Length 21;
Best Local Similarity 83.3%; Pred. No. 7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 36 GGAGCCTCAGTCACAGAGA 53
DB 20 GGAGCCTCAGTCCTCAGA 3

RESULT 1044
US-10-355-577-560795
; Sequence 560795, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 560795
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-560795

Query Match 0.6%; Score 13.2; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2075 ACTGTCCTAAGCAGGGG 2092
DB 4 ACTGTCGCAAGGAGGGG 21

RESULT 1045
US-08-529-190A-4
; Sequence 4, Application US/08529190A
; GENERAL INFORMATION:
; APPLICANT: Masucci, Maria G.
; TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES
; CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti
; STREET: 75 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,190A
; FILING DATE: 15-SEP-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Ph.D., Kathleen A
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: THERE-005AX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-9100
; TELEFAX: 617-345-9111
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-529-190A-4
```

```
US-60-353-987-560795
; Sequence 560795, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 560795
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-560795

Query Match 0.6%; Score 13.2; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2075 ACTGTCCTAAGCAGGGG 2092
DB 4 ACTGTCGCAAGGAGGGG 21

RESULT 1046
US-08-529-190A-4/c
; Sequence 4, Application US/08529190A
; GENERAL INFORMATION:
; APPLICANT: Masucci, Maria G.
; TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES
; CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti
; STREET: 75 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,190A
; FILING DATE: 15-SEP-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Ph.D., Kathleen A
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: THERE-005AX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-9100
; TELEFAX: 617-345-9111
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-529-190A-4
```

Query Match 0.6%; Score 13; DB 1; Length 24;
Best Local Similarity 76.2%; Pred. No. 8e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 296 TGCTCTGGAGCTGTGGTGG 316
||| ||||| ||||| |||||
Db 23 TGGTGCTGGAGGTGGGGTGG 3

RESULT 1047

US-08-733-369A-60/c
; Sequence 60, Application US/08733369A
; GENERAL INFORMATION:
; APPLICANT: Masucci, Maria G.
; TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES CONFERRING
; CORRESPONDENCE ADDRESS:
; STREET: Kathleen M. Williams, Banner & Witcoff, Ltd.
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,369A
; FILING DATE: 17 October, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/522,995
; FILING DATE: 01-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/529,190
; FILING DATE: 15-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 95013249
; FILING DATE: 10-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/SB96/00876
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 95-1391-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-9100
; TELEFAX: 617-345-9111
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-733-369A-60

Query Match 0.6%; Score 13; DB 1; Length 24;
Best Local Similarity 76.2%; Pred. No. 8e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 296 TGCTCTGGAGCTGTGGTGG 316
||| ||||| ||||| |||||
Db 23 TGGTGCTGGAGGTGGGGTGG 3

RESULT 1048

US-08-970-900-55/c
; Sequence 55, Application US/08970900
; GENERAL INFORMATION:

; APPLICANT: Masucci, Maria G.
; TITLE OF INVENTION: FUSION PROTEINS HAVING INCREASED HALF-LIVES.
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; STREET: Kathleen M. Williams, Banner & Witcoff, Ltd.
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02111

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,900
; FILING DATE: 14-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/030,986
; FILING DATE: 15-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/048,945
; FILING DATE: 25-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 3255/59831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-9100
; TELEFAX: 617-345-9111
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-970-900-55

Query Match 0.6%; Score 13; DB 1; Length 24;
Best Local Similarity 76.2%; Pred. No. 8e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 296 TGCTCTGGAGCTGTGGTGG 316
||| ||||| ||||| |||||
Db 23 TGGTGCTGGAGGTGGGGTGG 3

RESULT 1049

PCT-US02-25940-3485/c
; Sequence 3485, Application PC/TUS0225940
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25940
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 3485
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (437846)...(437861)
; OTHER INFORMATION: Chromosome = 1 Strand = negative
PCT-US02-25940-3485

Query Match 0.6%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1380 GCGGCGCCTAGGGCTG 1395
Db 16 GCGGCGGCGAGGGCTG 1

```

RESULT 1050
US-10-227-563-3485/c
; Sequence 3485, Application US/10227563
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Ziegler Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,563
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 3485
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (437846)...(437861)
; OTHER INFORMATION: Chromosome = 1 Strand = negative
US-10-227-563-3485

```

Query Match 0.6%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1380 GCGGCGCTAGGCTG 1395
Db 16 GCGGCGCGAGGCTG 1

```

RESULT 1051
US-10-367-892-3485/c
; Sequence 3485, Application US/10367892
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J ; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCES: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,892
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 3485
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (437846)...(437861)
; OTHER INFORMATION: Chromosome = 1 Strand = negative
US-10-367-892-3485

```

```

Query Match          0.6%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Qy 1380 GCGGCGCTAGGGCTG 1395
Db 16 GCGGCGCGAGGGCTG 1

RESULT 1052
US-10-310-188-35499/c
; Sequence 35499, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19

```

; NUMBER OF SEQ ID NOS: 86941
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35499
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-35499

```

```
Query Match          0.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 6.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1380 GCGGCCCTAGGGCTG 1395
db 16 GCGGCCGCGAGGGCTG 1

RESULT 1053
US-08-529-190A-7/c
; Sequence 7, Application US/08529190A
; GENERAL INFORMATION:
; APPLICANT: Masucci, Maria G.
; TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES
; TITLE OF INVENTION: CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM

CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Alleg
STREET: 75 State Street
CITY: Boston

STATE: MA
COUNTRY: USA
ZIP: 02109

```

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

```

```

; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: IIS/00/500 1 000

```

```

; FILING DATE: 15-SEP-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

```

```

RESULT 1054
US-08-733-369A-63/c
; Sequence 63, Application US/08733369A
; GENERAL INFORMATION:
; APPLICANT: Masucci, Maria G.
; TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES CONFERRING
; INVIBILITY TO THE IMMUNE SYSTEM.
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathleen M. Williams, Banner & Witcoff, Ltd.
; STREET: One Financial Center
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,369A
; FILING DATE: 17 October, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/522,995
; FILING DATE: 01-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/529,190
; FILING DATE: 15-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 95013249
; FILING DATE: 10-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00876
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 95-1391-D
; TELEPHONE: 617-345-9100
; TELEFAX: 617-345-9111
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-733-369A-63

Query Match 0.6%; Score 12.8; DB 1; Length 24;
Best Local Similarity 70.8%; Pred. No. 8.5e+02;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 295 GTGCTCTGGAGCTGTGGTGGGA 318
Db 24 GTGGAGCTGGAGTGGCGGTGGAA 1

RESULT 1055
US-08-970-900-57/c
; Sequence 57, Application US/08970900
; GENERAL INFORMATION:
; APPLICANT: Masucci, Maria G.
; TITLE OF INVENTION: FUSION PROTEINS HAVING INCREASED HALF-LIVES.
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathleen M. Williams, Banner & Witcoff, Ltd.
; STREET: One Financial Center
; CITY: Boston
; STATE: Massachusetts

```

```

; COUNTRY: USA
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,900
; FILING DATE: 14-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/030,986
; FILING DATE: 15-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/048,945
; FILING DATE: 25-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 3255/59831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-9100
; TELEFAX: 617-345-9111
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-970-900-57

Query Match 0.6%; Score 12.8; DB 1; Length 24;
Best Local Similarity 70.8%; Pred. No. 8.5e+02;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 295 GTGCTCTGGAGCTGTGGTGGGA 318
Db 24 GTGGAGCTGGAGTGGCGGTGGAA 1

RESULT 1056
PCT-US02-34679-162
; Sequence 162, Application PC/TUS0234679
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308PC
; CURRENT APPLICATION NUMBER: PCT/US02/34679
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28

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; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
PCT-US02-34679-162
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Query Match 0.6%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 7.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1081 ACTCCAGGCTTCAC 1094
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Db 2 ACTCCAGGCTTCTC 15
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RESULT 1057
US-10-282-174-162
; Sequence 162, Application US/10282174
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308
; CURRENT APPLICATION NUMBER: US/10/282,174
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-282-174-162
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Query Match 0.6%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 7.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1081 ACTCCAGGCTTCAC 1094
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Db 2 ACTCCAGGCTTCTC 15
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RESULT 1058
US-10-600-009-162
; Sequence 162, Application US/10600009
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; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308B
; CURRENT APPLICATION NUMBER: US/10/600,009
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/282,174
; PRIOR FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-600-009-162
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```
Query Match 0.6%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 7.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1081 ACTCCAGGCTTCAC 1094
||| |||||
Db 2 ACTCCAGGCTTCTC 15
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RESULT 1059
PCT-US02-29102-30/c
; Sequence 30, Application PC/TUS0229102
; GENERAL INFORMATION:
; APPLICANT: Applied Biosystems
; APPLICANT: Bolchakova, Elena V.
; APPLICANT: Rozzelle, James E.
; TITLE OF INVENTION: A Novel DNA Polymerase from the Thermophilic Thermus Scotoeductu
; FILE REFERENCE: 1560.002W01
; CURRENT APPLICATION NUMBER: PCT/US02/29102
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/334489
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/322218
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Thermus scotoeductus
PCT-US02-29102-30
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Query Match 0.6%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 301 CTGGAGCTGTTGGTGGG 317
Db 17 CTGGAGGTGGAGGTGGG 1

RESULT 1060

PCT-US02-37657-51/c
; Sequence 51, Application PC/TUS0237657
; GENERAL INFORMATION:
; APPLICANT: APPLERA CORPORATION
; APPLICANT: ROZZELLE, James
; APPLICANT: BOLCHAKOVA, Elena
; TITLE OF INVENTION: THERMUS BROCKIANUS NUCLEIC ACID POLYMERASES
; FILE REFERENCE: 4768WO
; CURRENT APPLICATION NUMBER: PCT/US02/37657
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: 60/334,434
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Thermus brockianus
PCT-US02-37657-51

Query Match 0.6%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 301 CTGGAGCTGTTGGTGGG 317
Db 17 CTGGAGGTGGAGGTGGG 1

RESULT 1061

PCT-US02-37764-30/c
; Sequence 30, Application PC/TUS0237764
; GENERAL INFORMATION:
; APPLICANT: APPLERA CORPORATION
; APPLICANT: ROZZELLE, James
; APPLICANT: BOLCHAKOVA, Elena
; TITLE OF INVENTION: Thermus Oshimai Nucleic Acid Polymerases
; FILE REFERENCE: 477WO
; CURRENT APPLICATION NUMBER: PCT/US02/37764
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/334,798
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Thermus oshimai
PCT-US02-37764-30

Query Match 0.6%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 301 CTGGAGCTGTTGGTGGG 317
Db 17 CTGGAGGTGGAGGTGGG 1

RESULT 1062

US-10-302-817A-51/c
; Sequence 51, Application US/10302817A
; GENERAL INFORMATION:

; APPLICANT: ROZZELLE, James
; APPLICANT: BOLCHAKOVA, Elena
; TITLE OF INVENTION: THERMUS BROCKIANUS NUCLEIC ACID POLYMERASES
; FILE REFERENCE: 4768US
; CURRENT APPLICATION NUMBER: US/10/302,817A
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: 60/334,434
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Thermus brockianus
US-10-302-817A-51

Query Match 0.6%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 301 CTGGAGCTGTTGGTGGG 317
Db 17 CTGGAGGTGGAGGTGGG 1

RESULT 1063

US-10-303-109A-30/c
; Sequence 30, Application US/10303109A
; GENERAL INFORMATION:
; APPLICANT: BOLCHAKOVA, Elena
; APPLICANT: ROZZELLE, James
; TITLE OF INVENTION: Thermus Oshimai Nucleic Acid Polymerases
; FILE REFERENCE: 477TUS
; CURRENT APPLICATION NUMBER: US/10/303,109A
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/334,798
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Thermus oshimai
US-10-303-109A-30

Query Match 0.6%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 301 CTGGAGCTGTTGGTGGG 317
Db 17 CTGGAGGTGGAGGTGGG 1

Search completed: March 1, 2004, 15:37:18
Job time : 29 secs

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PAVCO,
PI DENNIS MACEJAK
PC C12N9/00.A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
CC hepatitis C virus infection.
FH Key Location/Qualifiers
FT source 1..14
FT /organism='Hepatitis virus (hepatitis C FT
virus)'
FEATURES
Location/Qualifiers
1..14
/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
Query Match 0.5%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 6.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1177 GCGGCTCCCGC 1188
DB 3 GCGGCTCCCGC 14
RESULT 1274
BD209419 14 bp RNA linear PAT 17-JUL-2003
LOCUS Enzymatic nucleic acid treatment of diseases or conditions related
DEFINITION to hepatitis C virus infection.
ACCESSION BD209419
VERSION BD209419.1 GI:33019189
KEYWORDS JP 2002512791-A/3009.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Blatt, L., McSwiggen, J.A., Roberts, B., Pavco, P.A. and Macejak, D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 3009 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/3009
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545391
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00.A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
CC hepatitis C virus infection.
FH Key Location/Qualifiers
FT source 1..14
FT /organism='Hepatitis virus (hepatitis C FT
virus)'
FEATURES
Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
Query Match 0.5%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 6.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1216 GGTGACCCCATC 1227
DB 3 GGTGACCCCATC 14
RESULT 1275
S81271 14 bp mRNA linear PRI 07-MAY-1993
LOCUS mitochondrial acetoacetyl-coenzyme A thiolase [human, mRNA Partial
DEFINITION Mutant, 14 nt].
ACCESSION S81271
VERSION S81271.1 GI:245356
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 14)
AUTHORS Fukao, I., Yamaguchi, S., Orii, T., Schutgens, R.B., Osumi, T. and Hashimoto, T.
TITLE Identification of three mutant alleles of the gene for mitochondrial acetoacetyl-coenzyme A thiolase. A complete analysis of two generations of a family with 3-ketothiolase deficiency
JOURNAL J. Clin. Invest. 89 (2), 474-479 (1992)
MEDLINE 92147861
PUBMED 1346617
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 81271] from the original journal article. This sequence comes from Figure 2.
COMMENT exon 8 skipping
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/gene="mitochondrial acetoacetyl-coenzyme A thiolase"
Query Match 0.5%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 6.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 919 CTTTGCCTTTTA 930
DB 13 CTTGCGCTTTTA 2
Search completed: March 1, 2004, 15:13:28
Job time : 29 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 1, 2004, 15:39:29 ; Search time 0.001 Seconds
(without alignments)
1456.514 Million cell updates/sec

Title: us-09-695-451-1
Perfect score: 9161
Sequence: 1 Gggcccgatctgaacc.....tacactaaattctgaagtt 2161

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 25 seqs, 337 residues
Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 8
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 44 summaries

Database : rnnp.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	18	0.8	18	1	US-10-774-118-15
C 2	14.8	0.7	21	1	Sequence 15, Appl
C 3	14.8	0.7	21	1	Sequence 23831, A
C 4	12.2	0.6	17	1	Sequence 23832, A
C 5	12.2	0.5	17	1	PCT-US03-31862-1271
C 6	11.8	0.5	15	1	PCT-US03-31862-1272
C 7	11.4	0.5	15	1	Sequence 16, Appl
C 8	11.2	0.5	16	1	Sequence 20, Appl
C 9	9.8	0.5	14	1	US-09-892-360-20
C 10	9.2	0.4	14	1	US-10-767-471-49917
C 11	9.2	0.4	14	1	PCT-US03-31862-2689
C 12	9	0.4	17	1	Sequence 2689, Ap
C 13	9	0.4	17	1	Sequence 20, Appl
C 14	8.8	0.4	12	1	Sequence 1271, Ap
C 15	8.8	0.4	12	1	Sequence 1272, Ap
C 16	8.8	0.4	12	1	Sequence 19, Appl
C 17	8.8	0.4	12	1	Sequence 19, Appl
C 18	8.8	0.4	12	1	US-10-484-991-19
C 19	8.8	0.4	12	1	US-10-484-991-25
C 20	8.8	0.4	12	1	US-10-484-991-80
C 21	8.8	0.4	12	1	US-10-451-323-4
C 22	8.6	0.4	16	1	US-10-767-471-49917
C 23	8.6	0.4	21	1	Sequence 15, Appl
C 24	8.4	0.4	21	1	Sequence 15, Appl
C 25	8.4	0.4	10	1	US-10-770-726-23831
C 26	8.4	0.4	10	1	Sequence 6, Appl
C 27	8.4	0.4	11	1	Sequence 7, Appl
C 28	8.4	0.4	11	1	US-10-652-361-6
C 29	8.4	0.4	11	1	US-10-652-361-7
C 30	8.4	0.4	12	1	US-10-652-430-7
C 31	8.4	0.4	12	1	US-10-660-897-38
C 32	8.4	0.4	12	1	US-10-660-897-32
C 33	8.4	0.4	12	1	US-10-484-991-25
C 34	8.4	0.4	12	1	US-10-484-991-10
C 35	8.4	0.4	12	1	PCT-US03-26191A-10
C 36	8.4	0.4	12	1	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-10-774-118-15/c
; GENERAL INFORMATION:
; APPLICANT: Le Junming
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975-1005-038
; CURRENT APPLICATION NUMBER: US/10/774,118
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: US 09/756,301
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR oligonucleotides
US-10-774-118-15

Query Match 0.8%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 TTGTGCTACCCAGATT 852
DB 18 TTGTGCTACCCAGATT 1

RESULT 2
US-10-770-726-23831/c


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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,066
; FILING DATE: 05-Jan-2001
; APPLICATION NUMBER: 06/848,013
; FILING DATE: 2001-05-07
; APPLICATION NUMBER: 07/830,886
; FILING DATE: 04-FEB-1992
; APPLICATION NUMBER: 07/748,277
; FILING DATE: 21-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kegan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 02939.04541
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-767-471-49916

Query Match          0.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.4;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 891 GCTGTTGCCCTGGT 905
Db 15 GCTGTGGCTCTGGT 1

RESULT 7
US-09-892-360-20/c
; Sequence 20, Application US/09892360
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LESAGE, FLORIAN
; APPLICANT: ROMBY, GEORGES
; TITLE OF INVENTION: HUMAN TREK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE
; TITLE OF INVENTION: K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND
; TITLE OF INVENTION: RLIZOLE
; FILE REFERENCE: 1256-R-00
; CURRENT APPLICATION NUMBER: US/09/892,360
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 60/214,559
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-892-360-20

Query Match          0.5%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 3.6;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 869 CTGAGGACTCAGG 881
Db 15 CTGAGGACTCAGG 3

RESULT 8
US-10-767-471-49917/c
; Sequence 49917, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49917
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-767-471-49917

Query Match          0.5%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 5.5;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1266 CTTCCAGAAGTGGGAG 1281
Db 16 CTTCCAGAAGCGGGAG 1

RESULT 9
PCT-US03-31862-2689
; Sequence 2689, Application PC/TUS0331862
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF DELAWARE
; APPLICANT: KMEC, ERIC B.
; APPLICANT: VAN BRABANT, ANJA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN
; TITLE OF INVENTION: OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION
; FILE REFERENCE: NaPro-18 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/31862
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: US 60/453,360
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/416,983
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 2707
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2689
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-31862-2689

Query Match          0.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 12;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 880 GGCACCACAGTGC 892
Db 1 GACACCACGGTGC 13

RESULT 10
PCT-US03-31862-2689/c
; Sequence 2689, Application PC/TUS0331862
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF DELAWARE
; APPLICANT: KMEC, ERIC B.
; APPLICANT: VAN BRABANT, ANJA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN
; TITLE OF INVENTION: OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION
; FILE REFERENCE: NaPro-18 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/31862
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: US 60/453,360
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/416,983
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 2707
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2689
```


; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-31862-2689

Query Match 0.4%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 19;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1822 TGCCCGCTGGGCTC 1835
Db ||| ||||| |||
14 TGCACCGTGGGTGC 1

RESULT 11

US-09-892-360-20
; Sequence 20, Application US/09892360
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LESAGE, FLORIAN
; APPLICANT: ROMEY, GEORGES
; TITLE OF INVENTION: HUMAN TREK2, A STRETCH-AND APARCHIDONIC ACID-SENSITIVE
; TITLE OF INVENTION: K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND
; TITLE OF INVENTION: RILUZOLE
; FILE REFERENCE: 1256-R-00
; CURRENT APPLICATION NUMBER: US/09/892,360
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 60/214,559
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-892-360-20

Query Match 0.4%; Score 9.2; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 23;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1606 CCCAGTCTTCTCAG 1619
Db ||| ||||| |||||
2 CCCTGACTCTTCAG 15

RESULT 12

PCT-US03-31862-1271
; Sequence 1271, Application PC/TUS0331862
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF DELAWARE
; APPLICANT: KMEC, ERIC B.
; APPLICANT: VAN BRABANT, ANJA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN
; TITLE OF INVENTION: OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION
; FILE REFERENCE: Napro-18 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/31862
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: US 60/453,360
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/416,983
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 2707
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1271
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Triticum aestivum
PCT-US03-31862-1271

Query Match 0.4%; Score 9; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 32;
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 864 GGGCACTGAGGACTCAG 880
Db ||| ||||| |||||
1 GGCAGCTGAGTCGTGTCAG 17

RESULT 13

PCT-US03-31862-1272/C
; Sequence 1272, Application PC/TUS0331862
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF DELAWARE
; APPLICANT: KMEC, ERIC B.
; APPLICANT: VAN BRABANT, ANJA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN
; TITLE OF INVENTION: OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION
; FILE REFERENCE: Napro-18 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/31862
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: US 60/453,360
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/416,983
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 2707
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1272
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Triticum aestivum
PCT-US03-31862-1272

Query Match 0.4%; Score 9; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 32;
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 864 GGGCACTGAGGACTCAG 880
Db ||| ||||| |||||
17 GGCAGCTGAGTCGTGTCAG 1

RESULT 14

US-10-484-991-19
; Sequence 19, Application US/10484991
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Klinman, Dennis M.
; APPLICANT: Gursel, Ihsan
; APPLICANT: Puri, Raj K.
; APPLICANT: Kawakami, Koji
; APPLICANT: Ishii, Ken J.
; APPLICANT: Joshi, Bharat H.
; TITLE OF INVENTION: USE OF STERICALLY STABILIZED CATIONIC LIPOSOMES TO EFFICIENTLY
; TITLE OF INVENTION: DELIVER CPG OLIGONUCLEOTIDES IN VIVO
; FILE REFERENCE: 4239-67620
; CURRENT APPLICATION NUMBER: US/10/484,991
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 60/308,283
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US02/24235
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cpg oligodeoxynucleotide
US-10-484-991-19

Query Match 0.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 16;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1083 TCCAGGCTTCAC 1094
||| |||||
Db 1 TCGAGGCTTCTC 12

RESULT 15

US-10-484-991-19/c
; Sequence 19, Application US/10484991
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Klinman, Dennis M.
; APPLICANT: Gursel, Ihsan
; APPLICANT: Puri, Raj K.
; APPLICANT: Kawakami, Koji
; APPLICANT: Ishii, Ken J.
; APPLICANT: Joshi, Bharat H.
; TITLE OF INVENTION: USE OF STERICALLY STABILIZED CATIONIC LIPOSOMES TO EFFICIENTLY
; FILE REFERENCE: 4239-67620
; CURRENT FILING DATE: 2004-01-26
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 60/308,283
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US02/24235
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CpG oligodeoxynucleotide
US-10-484-991-19

Query Match 0.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 813 GAAAGCGCTGGA 824
||| |||||
Db 12 GAGAAGCCTCGA 1

RESULT 16

US-10-484-991-23/c
; Sequence 23, Application US/10484991
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Klinman, Dennis M.
; APPLICANT: Gursel, Ihsan
; APPLICANT: Puri, Raj K.
; APPLICANT: Kawakami, Koji
; APPLICANT: Ishii, Ken J.
; APPLICANT: Joshi, Bharat H.
; TITLE OF INVENTION: USE OF STERICALLY STABILIZED CATIONIC LIPOSOMES TO EFFICIENTLY
; FILE REFERENCE: 4239-67620
; CURRENT FILING DATE: 2004-01-26
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 60/308,283
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US02/24235
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23

; LENGTH: 12

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CpG oligodeoxynucleotide
US-10-484-991-23

Query Match 0.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1282 GACAGCGCCAC 1293
||| |||||
Db 1 12 GTCAGCGCCGAC 1

RESULT 17

US-10-484-991-25
; Sequence 25, Application US/10484991
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Klinman, Dennis M.
; APPLICANT: Gursel, Ihsan
; APPLICANT: Puri, Raj K.
; APPLICANT: Kawakami, Koji
; APPLICANT: Ishii, Ken J.
; APPLICANT: Joshi, Bharat H.
; TITLE OF INVENTION: USE OF STERICALLY STABILIZED CATIONIC LIPOSOMES TO EFFICIENTLY
; FILE REFERENCE: 4239-67620
; CURRENT FILING DATE: 2004-01-26
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 60/308,283
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US02/24235
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CpG oligodeoxynucleotide
US-10-484-991-25

Query Match 0.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1282 GACAGCGCCAC 1293
||| |||||
Db 1 GTCAGCGCCGAC 12

RESULT 18

US-10-484-991-80/c
; Sequence 80, Application US/10484991
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Klinman, Dennis M.
; APPLICANT: Gursel, Ihsan
; APPLICANT: Puri, Raj K.
; APPLICANT: Kawakami, Koji
; APPLICANT: Ishii, Ken J.
; APPLICANT: Joshi, Bharat H.
; TITLE OF INVENTION: USE OF STERICALLY STABILIZED CATIONIC LIPOSOMES TO EFFICIENTLY
; FILE REFERENCE: 4239-67620

```
; CURRENT APPLICATION NUMBER: US/10/484,991
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 60/308,283
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US02/24235
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CpG oligodeoxynucleotide
US-10-484-991-80

Query Match      0.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1027 GAGCTTGAAGGA 1038
Db 12 GAGCTGAAGCA 1

RESULT 19
US-10-451-323-4/c
; Sequence 4, Application US/10451323
; GENERAL INFORMATION:
; APPLICANT: MARCHAL, GILLES
; APPLICANT: ROMAIN, FELIX
; APPLICANT: PESCHER, PASCALE
; TITLE OF INVENTION: IMMUNOGENIC GLYCOPETIDES, SCREENING, PREPARATION AND USES
; FILE REFERENCE: 238218US0PCT
; CURRENT APPLICATION NUMBER: US/10/451,323
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: PCT/FR01/04100
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: FR 00/16808
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-10-451-323-4

Query Match      0.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1166 GTCCCAACTTTG 1177
Db 12 GGCCCAAGCTG 1

RESULT 20
US-10-767-471-49917
; Sequence 49917, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49917
; LENGTH: 16
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-767-471-49917

Query Match      0.4%; Score 8.8; DB 1; Length 16;
Best Local Similarity 83.3%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 524 CCGCTTCAGAAA 535
Db 4 CCGCTTCTGGAA 15

RESULT 21
US-10-774-118-15
; Sequence 15, Application US/10774118
; GENERAL INFORMATION:
; APPLICANT: Le, Junning
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: 0975.1005-038
; CURRENT APPLICATION NUMBER: US/10/774,118
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 09/756,301
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR oligonucleotides
US-10-774-118-15

Query Match      0.4%; Score 8.6; DB 1; Length 18;
Best Local Similarity 73.3%; Pred. No. 36;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1441 CTGCGCGAGGCGCAA 1455
Db 4 CTGGGGTAGGCACAA 18

RESULT 22
US-10-770-726-23831
; Sequence 23831, Application US/10770726
; GENERAL INFORMATION:
; APPLICANT: Wyeth
```

```
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23831
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-23831

Query Match      0.4%; Score 8.6; DB 1; Length 21;
Best Local Similarity 73.3%; Pred. No. 32;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1519 GGACGGCGTCTCCGC 1533
Db 7 GCACGAGTCTCAGC 21

RESULT 23
US-10-770-726-23832
; Sequence 23832, Application US/10770726
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23832
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAI
US-10-770-726-23832

Query Match      0.4%; Score 8.6; DB 1; Length 21;
Best Local Similarity 60.0%; Pred. No. 32;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1519 GGACGGCGTCTCCGC 1533
Db 5 GCACGAGUCCUACG 19

RESULT 24
US-10-652-361-6
; Sequence 6, Application US/10652361
; GENERAL INFORMATION:
; APPLICANT: WOUDENBERG, TIMOTHY M.
; APPLICANT: BAHATT, DAR
; APPLICANT: SHARAF, MUHAMMAD A.
; APPLICANT: LIU, TIMOTHY Z.
; APPLICANT: ERMAKOV, SERGUEI
; APPLICANT: CONNELL, CHARLES R.
; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND KITS FOR ASSEMBLING PROBES
; FILE REFERENCE: 5049 US
; CURRENT APPLICATION NUMBER: US/10/652,361
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-652-361-6

Query Match      0.4%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 75 AGAGGAGGGG 84
Db 1 AGAGGAGGAG 10

RESULT 25
US-10-652-361-7/c
; Sequence 7, Application US/10652361
; GENERAL INFORMATION:
; APPLICANT: WOUDENBERG, TIMOTHY M.
; APPLICANT: BAHATT, DAR
; APPLICANT: SHARAF, MUHAMMAD A.
; APPLICANT: LIU, TIMOTHY Z.
; APPLICANT: ERMAKOV, SERGUEI
; APPLICANT: CONNELL, CHARLES R.
; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND KITS FOR ASSEMBLING PROBES
; FILE REFERENCE: 5049 US
; CURRENT APPLICATION NUMBER: US/10/652,361
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-652-361-7

Query Match      0.4%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 75 AGAGGAGGGG 84
Db 10 AGAGGAGGAG 1

RESULT 26
US-10-652-430-6
; Sequence 6, Application US/10652430
; GENERAL INFORMATION:
; APPLICANT: WOUDENBERG, TIMOTHY M.
; APPLICANT: BAHATT, DAR
; APPLICANT: SHARAF, MUHAMMAD A.
; APPLICANT: LIU, TIMOTHY Z.
; APPLICANT: ERMAKOV, SERGUEI
; APPLICANT: CONNELL, CHARLES R.
; APPLICANT: HYLDIG-NIELSEN, JENS J.
; TITLE OF INVENTION: MULTIPLEX DETECTION COMPOSITIONS, METHODS, AND KITS
; FILE REFERENCE: 5023 US
; CURRENT APPLICATION NUMBER: US/10/652,430
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-652-430-6
```

Query Match 0.4%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 75 AGAGGAGGG 84
| | | | | | | | | |
Db 1 AGAGGAGG 10

RESULT 27
US-10-652-430-7/c
; Sequence 7, Application US/10652430
; GENERAL INFORMATION:
; APPLICANT: WOLDENBERG, TIMOTHY M.
; APPLICANT: BAHATT, DAR
; APPLICANT: SHARAF, MUHAMMAD A.
; APPLICANT: LIU, TIMOTHY Z.
; APPLICANT: ERMAKOV, SERGUEI
; APPLICANT: CONNELL, CHARLES R.
; APPLICANT: HYLDIG-NIELSEN, JENS J.
; TITLE OF INVENTION: MULTIPLEX DETECTION COMPOSITIONS, METHODS, AND KITS
; FILE REFERENCE: 5023 US
; CURRENT APPLICATION NUMBER: US/10/652,430
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in Ver. 3.2
; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-652-430-7

Query Match 0.4%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 75 AGAGGAGGG 84
| | | | | | | | | |
Db 10 AGAGGAGG 1

RESULT 28
US-10-660-897-38
; Sequence 38, Application US/10660897
; GENERAL INFORMATION:
; APPLICANT: Jin, Cheng
; APPLICANT: Chung, Mary
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Whitten, Jeffrey
; APPLICANT: Farrell, Thomas
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
; FILE REFERENCE: 53223200800
; CURRENT APPLICATION NUMBER: US/10/660,897
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: 60/410,475
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: motif
US-10-660-897-38

Query Match 0.4%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 17;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1859 GAGGATGAGG 1868
| | | | | | | | | |
Db 2 GAGGAGGAGG 11

RESULT 29
US-10-660-897-38/c
; Sequence 38, Application US/10660897
; GENERAL INFORMATION:
; APPLICANT: Jin, Cheng
; APPLICANT: Chung, Mary
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Whitten, Jeffrey
; APPLICANT: Farrell, Thomas
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
; FILE REFERENCE: 53223200800
; CURRENT APPLICATION NUMBER: US/10/660,897
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: 60/410,475
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: motif
US-10-660-897-38

Query Match 0.4%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 933 CCTCTCTCTC 942
| | | | | | | | | |
Db 11 CCTCTCTCTC 2

RESULT 30
US-10-484-991-23
; Sequence 23, Application US/10484991
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Klinman, Dennis M.
; APPLICANT: Gursel, Ihsan
; APPLICANT: Puri, Raj K.
; APPLICANT: Kawakami, Koji
; APPLICANT: Ishii, Ken J.
; APPLICANT: Joshi, Bharat H.
; TITLE OF INVENTION: USE OF SPERICALLY STABILIZED CATIONIC LIPOSOMES TO EFFICIENTLY
; FILE REFERENCE: 4239-67620
; CURRENT APPLICATION NUMBER: US/10/484,991
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 60/308,283
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US02/24235
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 23
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CpG oligodeoxynucleotide
US-10-484-991-23

Query Match 0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1796 GTCAGCGCTG 1805
||| |||||
Db 1 GTCGGCGCTG 10

RESULT 31
US-10-484-991-25/c
; Sequence 25, Application US/10484991
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Klimman, Dennis M.
; APPLICANT: Gursel, Ihsan
; APPLICANT: Puri, Raj K.
; APPLICANT: Kawakami, Koji
; APPLICANT: Ishii, Ken J.
; APPLICANT: Joshi, Bharat H.
; TITLE OF INVENTION: USE OF STERICALLY STABILIZED CATIONIC LIPOSOMES TO EFFICIENTLY
; FILE REFERENCE: 4239-67620
; CURRENT APPLICATION NUMBER: US/10/484,991
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 60/308,283
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US02/24235
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CpG oligodeoxynucleotide
US-10-484-991-25

Query Match 0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1796 GTCAGCGCTG 1805
||| |||||
Db 12 GTCGGCGCTG 3

RESULT 32
PCT-US03-26191A-10/c
; Sequence 10, Application PC/TUS0326191A
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; APPLICANT: ARAI, AKIKO
; TITLE OF INVENTION: STARS - A MUSCLE-SPECIFIC ACTIN-BINDING PROTEIN
; FILE REFERENCE: MYOG:037WO
; CURRENT APPLICATION NUMBER: PCT/US03/26191A
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 60/404,706
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
PCT-US03-26191A-10

Query Match 0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1182 TCACGCGCAGA 1191
||| |||||
Db 12 TCACGCGCAGA 3

RESULT 33
US-10-484-991-50/c
; Sequence 50, Application US/10484991
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Klimman, Dennis M.
; APPLICANT: Gursel, Ihsan
; APPLICANT: Puri, Raj K.
; APPLICANT: Kawakami, Koji
; APPLICANT: Ishii, Ken J.
; APPLICANT: Joshi, Bharat H.
; TITLE OF INVENTION: USE OF STERICALLY STABILIZED CATIONIC LIPOSOMES TO EFFICIENTLY
; FILE REFERENCE: 4239-67620
; CURRENT APPLICATION NUMBER: US/10/484,991
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 60/308,283
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US02/24235
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CpG oligodeoxynucleotide
US-10-484-991-50

Query Match 0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1258 CCCAACCCCC 1267
||| |||||
Db 12 CCCAACGCC 3

RESULT 34
US-10-660-897-11
; Sequence 11, Application US/10660897
; GENERAL INFORMATION:
; APPLICANT: Jin, Cheng
; APPLICANT: Chung, Mary
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Whitten, Jeffrey
; APPLICANT: Farrell, Thomas
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
; FILE REFERENCE: QUADRUPLIX FORMING NUCLEIC ACIDS AND MODULATORS THEREOF
; CURRENT APPLICATION NUMBER: US/10/660,897
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: 60/410,475
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence

```
/
; FEATURE:
; OTHER INFORMATION: quadruplex forming sequence
US-10-660-897-11

Query Match      0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1859 GAGGATGAGG 1868
Db 2 GAGGAGGAGG 11

RESULT 35
US-10-660-897-11/c
; Sequence 11, Application US/10660897
; GENERAL INFORMATION:
; APPLICANT: Jin, Cheng
; APPLICANT: Chung, Mary
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Whitten, Jeffrey
; APPLICANT: Farrell, Thomas
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
; TITLE OF INVENTION: QUADRUPLIX FORMING NUCLEIC ACIDS AND MODULATORS THEREOF
; FILE REFERENCE: 532232000800
; CURRENT APPLICATION NUMBER: US/10/660,897
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: 60/410,475
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: quadruplex forming sequence
US-10-660-897-11

Query Match      0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 933 CCTCTCTCTC 942
Db 11 CCTCTCTCTC 2

RESULT 36
US-10-660-897-19/c
; Sequence 19, Application US/10660897
; GENERAL INFORMATION:
; APPLICANT: Jin, Cheng
; APPLICANT: Chung, Mary
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Whitten, Jeffrey
; APPLICANT: Farrell, Thomas
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
; TITLE OF INVENTION: QUADRUPLIX FORMING NUCLEIC ACIDS AND MODULATORS THEREOF
; FILE REFERENCE: 532232000800
; CURRENT APPLICATION NUMBER: US/10/660,897
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: 60/410,475
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-660-897-19

Query Match      0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1859 GAGGATGAGG 1868
Db 2 GAGGAGGAGG 11

RESULT 37
US-10-660-897-24
; Sequence 24, Application US/10660897
; GENERAL INFORMATION:
; APPLICANT: Jin, Cheng
; APPLICANT: Chung, Mary
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Whitten, Jeffrey
; APPLICANT: Farrell, Thomas
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
; TITLE OF INVENTION: QUADRUPLIX FORMING NUCLEIC ACIDS AND MODULATORS THEREOF
; FILE REFERENCE: 532232000800
; CURRENT APPLICATION NUMBER: US/10/660,897
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: 60/410,475
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-660-897-24

Query Match      0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1859 GAGGATGAGG 1868
Db 2 GAGGAGGAGG 11

RESULT 38
US-10-660-897-24/c
; Sequence 24, Application US/10660897
; GENERAL INFORMATION:
; APPLICANT: Jin, Cheng
; APPLICANT: Chung, Mary
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Whitten, Jeffrey
; APPLICANT: Farrell, Thomas
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
; TITLE OF INVENTION: QUADRUPLIX FORMING NUCLEIC ACIDS AND MODULATORS THEREOF
; FILE REFERENCE: 532232000800
; CURRENT APPLICATION NUMBER: US/10/660,897
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: 60/410,475
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-660-897-24

Query Match      0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1859 GAGGATGAGG 1868
Db 2 GAGGAGGAGG 11
```

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 933 CCTCCTCTTC 942

Db 11 CCTCCTCTTC 2

RESULT 39

US-10-660-897-32
; Sequence 32, Application US/10660897
; GENERAL INFORMATION:
; APPLICANT: Jin, Cheng
; APPLICANT: Chung, Mary
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Whitten, Jeffrey
; APPLICANT: Farrell, Thomas
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
; TITLE OF INVENTION: QUADRUPLIX FORMING NUCLEIC ACIDS AND MODULATORS THEREOF
; FILE REFERENCE: 53223200800
; CURRENT APPLICATION NUMBER: US/10/660,897
; CURRENT FILING DATE: 2003-09-11
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: motif
US-10-660-897-32

Query Match 0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1859 GAGGATGAGG 1868

Db 2 GAGGAGGAGG 11

RESULT 40

US-10-660-897-32/c
; Sequence 32, Application US/10660897
; GENERAL INFORMATION:
; APPLICANT: Jin, Cheng
; APPLICANT: Chung, Mary
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Whitten, Jeffrey
; APPLICANT: Farrell, Thomas
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
; TITLE OF INVENTION: QUADRUPLIX FORMING NUCLEIC ACIDS AND MODULATORS THEREOF
; FILE REFERENCE: 53223200800
; CURRENT APPLICATION NUMBER: US/10/660,897
; CURRENT FILING DATE: 2003-09-11
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: motif
US-10-660-897-32

Query Match 0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 933 CCTCCTCTTC 942

Db 11 CCTCCTCTTC 2

RESULT 41

US-10-652-361-6/c
; Sequence 6, Application US/10652361
; GENERAL INFORMATION:
; APPLICANT: WOUDEBERG, TIMOTHY M.
; APPLICANT: BAHATT, DAR
; APPLICANT: SHARAF, MUHAMMAD A.
; APPLICANT: LIU, TIMOTHY Z.
; APPLICANT: ERMAKOV, SERGUEI
; APPLICANT: CONNELL, CHARLES R.
; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND KITS FOR ASSEMBLING PROBES
; FILE REFERENCE: 5049 US
; CURRENT APPLICATION NUMBER: US/10/652,361
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-652-361-6

Query Match 0.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 933 CCTCCTCTTC 940

Db 8 CCTCCTCTTC 1

RESULT 42

US-10-652-361-7
; Sequence 7, Application US/10652361
; GENERAL INFORMATION:
; APPLICANT: WOUDEBERG, TIMOTHY M.
; APPLICANT: BAHATT, DAR
; APPLICANT: SHARAF, MUHAMMAD A.
; APPLICANT: LIU, TIMOTHY Z.
; APPLICANT: ERMAKOV, SERGUEI
; APPLICANT: CONNELL, CHARLES R.
; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND KITS FOR ASSEMBLING PROBES
; FILE REFERENCE: 5049 US
; CURRENT APPLICATION NUMBER: US/10/652,361
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-652-361-7

Query Match 0.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 933 CCTCCTCTTC 940

Db 3 CCTCCTCTTC 10

RESULT 43


```
US-10-652-430-6/c
; Sequence 6, Application US/10652430
; GENERAL INFORMATION:
; APPLICANT: WOUDEBERG, TIMOTHY M.
; APPLICANT: BAHATT, DAR
; APPLICANT: SHARAF, MUHAMMAD A.
; APPLICANT: LIU, TIMOTHY Z.
; APPLICANT: ERMAKOV, SERGUEI
; APPLICANT: CONNELL, CHARLES R.
; APPLICANT: HYLDIG-NIELSEN, JENS J.
; TITLE OF INVENTION: MULTIPLEX DETECTION COMPOSITIONS, METHODS, AND KITS
; FILE REFERENCE: 5023 US
; CURRENT APPLICATION NUMBER: US/10/652,430
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-652-430-6

Query Match          0.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 933 CCTCCTCT 940
Db 8 CCTCCTCT 1

RESULT 44
US-10-652-430-7
; Sequence 7, Application US/10652430
; GENERAL INFORMATION:
; APPLICANT: WOUDEBERG, TIMOTHY M.
; APPLICANT: BAHATT, DAR
; APPLICANT: SHARAF, MUHAMMAD A.
; APPLICANT: LIU, TIMOTHY Z.
; APPLICANT: ERMAKOV, SERGUEI
; APPLICANT: CONNELL, CHARLES R.
; APPLICANT: HYLDIG-NIELSEN, JENS J.
; TITLE OF INVENTION: MULTIPLEX DETECTION COMPOSITIONS, METHODS, AND KITS
; FILE REFERENCE: 5023 US
; CURRENT APPLICATION NUMBER: US/10/652,430
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-652-430-7

Query Match          0.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 933 CCTCCTCT 940
Db 3 CCTCCTCT 10

Search completed: March 1, 2004, 15:39:30
Job time : 0.001 secs
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2004, 15:41:44 ; Search time 1 Seconds
(without alignments)

3.916 Million cell updates/sec

Title: us-09-695-451-1

Perfect score: 2161

Sequence: 1 cggccagtgatctgaacc.....tacactaaattctgaagtt 2161

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 91 seqs, 906 residues

Total number of hits satisfying chosen parameters: 182

Minimum DB seq length: 8

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 170 summaries

Database : rst.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	16.4	0.8	19	1	ACCESSION:AZ788326
C 2	11.4	0.5	14	1	ACCESSION:CA798290
C 3	11.4	0.5	16	1	ACCESSION:AL696566
C 4	11	0.5	12	1	ACCESSION:BH169696
C 5	10.2	0.5	16	1	ACCESSION:AL696566
C 6	10	0.5	19	1	ACCESSION:AZ788326
C 7	9.8	0.5	13	1	ACCESSION:BQ589768
C 8	9.8	0.5	13	1	ACCESSION:BH170808
C 9	9.4	0.4	12	1	ACCESSION:BG925521
C 10	9.4	0.4	13	1	ACCESSION:BG926067
C 11	9.4	0.4	13	1	ACCESSION:BQ59423
C 12	9	0.4	9	1	ACCESSION:CF307276
C 13	9	0.4	9	1	ACCESSION:CF307431
C 14	9	0.4	11	1	ACCESSION:CF339065
C 15	9	0.4	11	1	ACCESSION:CF339065
C 16	9	0.4	11	1	ACCESSION:BQ585943
C 17	9	0.4	11	1	ACCESSION:BQ593914
C 18	9	0.4	12	1	ACCESSION:BQ592925
C 19	9	0.4	12	1	ACCESSION:BQ594497
C 20	9	0.4	12	1	ACCESSION:BQ594497
C 21	8.8	0.4	12	1	ACCESSION:BQ595544
C 22	8.8	0.4	12	1	ACCESSION:BQ587870
C 23	8.8	0.4	12	1	ACCESSION:BQ592925
C 24	8.8	0.4	12	1	ACCESSION:BQ594497
C 25	8.8	0.4	12	1	ACCESSION:BQ595544
C 26	8.8	0.4	13	1	ACCESSION:CF282215
C 27	8.8	0.4	13	1	ACCESSION:BG926067
C 28	8.4	0.4	10	1	ACCESSION:CF921234
C 29	8.4	0.4	10	1	ACCESSION:CK298980
C 30	8.4	0.4	11	1	ACCESSION:BM395228
C 31	8.4	0.4	11	1	ACCESSION:BQ590709
C 32	8.4	0.4	11	1	ACCESSION:BM395226
C 33	8.4	0.4	12	1	ACCESSION:BQ587288

ACCESSION:BQ587706	1	12	0.4	8.4	34	C
ACCESSION:BQ589761	1	12	0.4	8.4	35	C
ACCESSION:BQ591624	1	12	0.4	8.4	36	C
ACCESSION:AQ050979	1	12	0.4	8.4	37	C
ACCESSION:B07312	1	12	0.4	8.4	38	C
ACCESSION:CF339091	8	8	0.4	8	39	C
ACCESSION:CF277997	8	8	0.4	8	40	C
ACCESSION:CF301888	8	8	0.4	8	41	C
ACCESSION:CF302851	8	8	0.4	8	42	C
ACCESSION:CF312818	8	8	0.4	8	43	C
ACCESSION:CF309109	9	9	0.4	8	44	C
ACCESSION:CF312817	9	9	0.4	8	45	C
ACCESSION:CF318771	9	9	0.4	8	46	C
ACCESSION:CF330649	9	9	0.4	8	47	C
ACCESSION:CF333615	10	10	0.4	8	48	C
ACCESSION:CA794390	10	10	0.4	8	49	C
ACCESSION:CF322692	11	11	0.4	8	50	C
ACCESSION:BG925521	12	12	0.4	8	51	C
ACCESSION:BQ587288	12	12	0.4	8	52	C
ACCESSION:BQ587706	12	12	0.4	8	53	C
ACCESSION:BQ595423	13	13	0.4	8	54	C
ACCESSION:BG927412	11	11	0.4	7.8	55	C
ACCESSION:BG927896	11	11	0.4	7.8	56	C
ACCESSION:BM395997	11	11	0.4	7.8	57	C
ACCESSION:BM395997	11	11	0.4	7.8	58	C
ACCESSION:BQ585943	11	11	0.4	7.8	59	C
ACCESSION:BQ593914	11	11	0.4	7.8	60	C
ACCESSION:BU238234	11	11	0.4	7.8	61	C
ACCESSION:CF323154	11	11	0.4	7.8	62	C
ACCESSION:CF543031	11	11	0.4	7.8	63	C
ACCESSION:BQ587870	12	12	0.4	7.8	64	C
ACCESSION:BQ589761	12	12	0.4	7.8	65	C
ACCESSION:B07312	12	12	0.4	7.8	66	C
ACCESSION:AL394689	9	9	0.3	7.6	67	C
ACCESSION:CF307276	9	9	0.3	7.6	68	C
ACCESSION:CF307431	9	9	0.3	7.4	69	C
ACCESSION:CA850813	9	9	0.3	7.4	70	C
ACCESSION:CF313414	9	9	0.3	7.4	71	C
ACCESSION:CF313414	9	9	0.3	7.4	72	C
ACCESSION:CF323490	9	9	0.3	7.4	73	C
ACCESSION:CF307092	9	9	0.3	7.4	74	C
ACCESSION:CF322585	9	9	0.3	7.4	75	C
ACCESSION:CF322585	9	9	0.3	7.4	76	C
ACCESSION:CF325534	9	9	0.3	7.4	77	C
ACCESSION:CF325534	9	9	0.3	7.4	78	C
ACCESSION:CF325652	9	9	0.3	7.4	79	C
ACCESSION:CF325652	9	9	0.3	7.4	80	C
ACCESSION:BG925375	10	10	0.3	7.4	81	C
ACCESSION:BM396082	10	10	0.3	7.4	82	C
ACCESSION:BM396082	10	10	0.3	7.4	83	C
ACCESSION:BM396082	10	10	0.3	7.4	84	C
ACCESSION:BQ789997	10	10	0.3	7.4	85	C
ACCESSION:CF311011	10	10	0.3	7.4	86	C
ACCESSION:CF311011	10	10	0.3	7.4	87	C
ACCESSION:CA794390	10	10	0.3	7.4	88	C
ACCESSION:BM395226	11	11	0.3	7.4	89	C
ACCESSION:BH169696	12	12	0.3	7.4	90	C
ACCESSION:BQ591624	12	12	0.3	7.4	91	C
ACCESSION:CF339091	8	8	0.3	7	92	C
ACCESSION:CF295648	8	8	0.3	7	93	C
ACCESSION:CF921494	8	8	0.3	7	94	C
ACCESSION:CA851350	8	8	0.3	7	95	C
ACCESSION:CF313731	8	8	0.3	7	96	C
ACCESSION:CA851674	9	9	0.3	7	97	C
ACCESSION:BM396043	10	10	0.3	7	98	C
ACCESSION:BM396043	10	10	0.3	7	99	C
ACCESSION:CF323895	10	10	0.3	7	100	C
ACCESSION:CF323895	10	10	0.3	7	101	C
ACCESSION:CF336905	10	10	0.3	7	102	C
ACCESSION:BM395228	11	11	0.3	7	103	C
ACCESSION:BG927412	11	11	0.3	7	104	C
ACCESSION:BG927896	11	11	0.3	7	105	C
ACCESSION:CF323154	11	11	0.3	7	106	C
ACCESSION:CF282215	12	12	0.3	7	107	C

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c 107 6.8 0.3 10 1 BG925375
c 108 6.8 0.3 10 1 CF333615
c 109 6.8 0.3 10 1 ACCESSION:CF333615
c 110 6.8 0.3 11 1 ACCESSION:CF336905
c 111 6.8 0.3 11 1 ACCESSION:BQ590709
c 112 6.8 0.3 11 1 ACCESSION:CF322692
c 113 6.8 0.3 12 1 ACCESSION:AQ050979
c 114 6.8 0.3 12 1 ACCESSION:BH170808
c 115 6.8 0.3 13 1 ACCESSION:CF798290
c 116 6.4 0.3 8 1 CF305141
c 117 6.4 0.3 8 1 ACCESSION:CF305141
c 118 6.4 0.3 8 1 ACCESSION:CF306116
c 119 6.4 0.3 8 1 ACCESSION:CF306116
c 120 6.4 0.3 8 1 ACCESSION:CF306762
c 121 6.4 0.3 8 1 ACCESSION:CF306762
c 122 6.4 0.3 8 1 ACCESSION:CF322514
c 123 6.4 0.3 8 1 ACCESSION:CF322514
c 124 6.4 0.3 8 1 ACCESSION:CF322653
c 125 6.4 0.3 8 1 ACCESSION:CF323889
c 126 6.4 0.3 8 1 ACCESSION:CF323889
c 127 6.4 0.3 8 1 ACCESSION:CF324406
c 128 6.4 0.3 8 1 ACCESSION:CF324406
c 129 6.4 0.3 8 1 ACCESSION:CF325379
c 130 6.4 0.3 8 1 ACCESSION:CF325379
c 131 6.4 0.3 8 1 ACCESSION:CF325469
c 132 6.4 0.3 8 1 ACCESSION:CF325469
c 133 6.4 0.3 8 1 ACCESSION:CF325485
c 134 6.4 0.3 8 1 ACCESSION:CF325485
c 135 6.4 0.3 8 1 ACCESSION:CF338362
c 136 6.4 0.3 8 1 ACCESSION:CF339016
c 137 6.4 0.3 8 1 ACCESSION:CF339699
c 138 6.4 0.3 8 1 ACCESSION:CF340204
c 139 6.4 0.3 8 1 ACCESSION:CF340204
c 140 6.4 0.3 8 1 ACCESSION:CF321494
c 141 6.4 0.3 8 1 ACCESSION:CA794554
c 142 6.4 0.3 8 1 ACCESSION:CA794554
c 143 6.4 0.3 9 1 ACCESSION:CA850813
c 144 6.4 0.3 9 1 ACCESSION:CF323490
c 145 6.4 0.3 9 1 ACCESSION:CA794225
c 146 6.4 0.3 9 1 ACCESSION:CA850899
c 147 6.4 0.3 9 1 ACCESSION:CA850899
c 148 6.4 0.3 9 1 ACCESSION:CF307008
c 149 6.4 0.3 9 1 ACCESSION:CF307008
c 150 6.4 0.3 9 1 ACCESSION:CF309109
c 151 6.4 0.3 9 1 ACCESSION:CF323636
c 152 6.4 0.3 9 1 ACCESSION:CF323636
c 153 6.4 0.3 9 1 ACCESSION:CF325619
c 154 6.4 0.3 9 1 ACCESSION:CF325619
c 155 6.4 0.3 10 1 ACCESSION:CF321234
c 156 6.4 0.3 10 1 ACCESSION:CK298980
c 157 6.4 0.3 11 1 ACCESSION:BU238234
c 158 6.2 0.3 11 1 CF543031
c 159 6 0.3 8 1 ACCESSION:CF338362
c 160 6 0.3 8 1 ACCESSION:CF339016
c 161 6 0.3 8 1 ACCESSION:CF339699
c 162 6 0.3 8 1 ACCESSION:CF340204
c 163 6 0.3 8 1 ACCESSION:CA850825
c 164 6 0.3 8 1 ACCESSION:CA850825
c 165 6 0.3 8 1 ACCESSION:CA851350
c 166 6 0.3 8 1 ACCESSION:CF297970
c 167 6 0.3 8 1 ACCESSION:CF297970
c 168 6 0.3 8 1 CF313731
c 169 6 0.3 8 1 ACCESSION:CF330558
c 170 6 0.3 8 1 CF330558

```

ALIGNMENTS

```

RESULT 1
AZ788326/c 19 bp DNA linear GSS 16-FEB-2001
LOCUS AZ788326 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION 2M0035P16F

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

```

clone UUGC2M0035P16 F, genomic survey sequence.
AZ788326
AZ788326.1 GI:12928014
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0035 row: P column: 16
Seq primer: GGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0035P16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid RL. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

FEATURES

source

```

Query Match 0.8%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. NO. 0.0068;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 987 CTCATTCTTTGTGGAA 1004

DB 19 CTCATTCTTTGTGGAA 2

```

RESULT 2
CA798290
LOCUS
DEFINITION

```

```

CA798290 14 bp mRNA linear EST 05-DEC-2002
Cac BL 611 Cac BL (Bean and Leaf from Amelonardo type Cacao)
Theobroma cacao cDNA clone Cac BL_611 5', mRNA sequence.

```

```

ACCESSION CA798290
VERSION CA798290.1 GI:26055376
KEYWORDS EST.
SOURCE Theobroma cacao (cacao)
ORGANISM Theobroma cacao
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
          Theobroma.
REFERENCE 1 (bases 1 to 14)
AUTHORS Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,
         Retzel, E.R. and Jones, C.A.
TITLE Gene discovery and microarray analysis of cacao (Theobroma cacao
L.) varieties
JOURNAL Planta 216 (2), 255-264 (2002)
MEDLINE 22337596
PUBMED 12447539
COMMENT Contact: Jones, Paul
         3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
         Tel: +44 1664 416644
         Email: Paul.Jones@eu.affem.com
         Seq primer: T3.
FEATURES
    source
        1..14
            /organism="Theobroma cacao"
            /mol_type="mRNA"
            /strain="Amelonado type"
            /db_xref="taxon:3641"
            /clone="Cac BL 611"
            /tissue_type="Mature leaf and mature bean"
            /cell_type="Whole organ"
            /dev_stage="maturity"
            /lab_host="XU-1 Blue MRF"
            /clone_lib="Cac_BL (Bean and Leaf from Amelonado type
            Cacao)"
            /note="Vector: pBK-CMV; Bean and leaf tissue from an
            Amelonado type Cacao tree."
Query Match 0.5%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 0.99;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1143 CTCACCTATACC 1155
Db 1 CTCGCCCTATACC 13

RESULT 3
ACCESSION AI696566/c
LOCUS AI696566
DEFINITION tx60f06.x1 NCI_CGAP_Utl1 Homo sapiens cDNA clone IMAGE:2273987 3,
          similar to TR:Q15662 Q15662 TRANSFORMATION-RELATED PROTEIN ;, mRNA
          sequence.
ACCESSION AI696566
VERSION AI696566.1 GI:4984466
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 16)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
         Email: cgap@remail.nih.gov
         Tissue Procurement: Christopher Mokaluk, M.D., Ph.D., Michael R.
         Emerit-Buck, M.D., Ph.D.
         cDNA Library Preparation: Life Technologies, Inc.
         cDNA Library Arrayed by: Greg Lennon, Ph.D.
         DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert length: 1662 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES
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            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:2273987"
            /tissue_type="well-differentiated endometrial
            adenocarcinoma 7 pooled tumors"
            /lab_host="DH10B"
            /clone_lib="NCI_CGAP_Utl1"
            /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
            Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.
            Average insert size 1.75 kb. Life Technologies catalog #:
            11538-014"
Query Match 0.5%; Score 11.4; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 3;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 880 GGCACCACAGTGCT 893
Db 14 GCCACCACAGTGCT 1

RESULT 4
LOCUS BH169696
DEFINITION BH169696 12-bp DNA linear GSS 03-OCT-2001
          SALK_001766 Arabidopsis thaliana TDNA insertion lines Arabidopsis
          thaliana genomic clone SALK_001766, genomic survey sequence.
ACCESSION BH169696
VERSION BH169696.1 GI:15905071
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
          Arabidopsis thaliana
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 12)
AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
         Gadrinab, C., Jeske, A., Karnes, M., Kim, C.-J., Parker, H., Prednis, L.,
         Shinn, P., Zimmerman, J. and Ecker, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
          Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
          Salk Institute Genomic Analysis Laboratory (SIGAL)
          The Salk Institute for Biological Studies
          10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
          Tel: 858 453 4100 x1752
          Fax: 858 558 6379
          Email: ecker@salk.edu
          This is single pass sequence recovered from the left border of
          TDNA.
Class: TDNA tagged.
FEATURES
    source
        1..12
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /strain="Columbia 0"
            /db_xref="taxon:3702"
            /clone="SALK_001766"
            /note="PCR was performed on Arabidopsis thaliana lines
            each of which contains one or more TDNA insertion
            elements. The resultant fragment for each line was
            directly sequenced to determine the genomic sequence at
            the site of insertion. Details of the protocols used can

```

be found at http://signal.salk.edu/tdna_protocols.html

Query Match 0.5%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1055 TGGCCCCAAC 1065
|||||
Db 1 TGGCCCCAAC 11

RESULT 5
LOCUS AI696566 16 bp mRNA linear EST 16-DEC-1999
DEFINITION tx60f06.x1 NCI_CGAP Utl Homo sapiens cDNA clone IMAGE:2273987 3' similar to TR:Q15662 Q15662 TRANSFORMATION-RELATED PROTEIN ; , mRNA sequence.

ACCESSION AI696566

VERSION AI696566

KEYWORDS EST.

SOURCE AI696566.1 GI:4984466

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 16)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

Clone Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1662 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 1.

FEATURES Location/Qualifiers

1..16

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2273987"

/tissue_type="well-differentiated endometrial

adenocarcinoma, 7 pooled tumors"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_Utl"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.75 kb. Life Technologies catalog #:

11538-014"

Query Match 0.5%; Score 10.2; DB 1; Length 16;

Best Local Similarity 75.0%; Pred. No. 16;

Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 192 AGCACTGCGGTGCCA 207

|||||

Db 1 AGCACTGNGGTGCCA 16

RESULT 6

LOCUS AZ788326 19 bp DNA linear GSS 16-FEB-2001

DEFINITION 2M0035P16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0035P16 F, genomic survey sequence.

ACCESSION AZ788326

VERSION AZ788326.1 GI:12928014

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhauser, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0035 row: P column: 16

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0035P16"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42rv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.5%; Score 10; DB 1; Length 19;

Best Local Similarity 72.2%; Pred. No. 47;

Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 956 ATCGCTACCAACGGTGA 973

|||||

Db 1 ATTCCCAACCAATGGA 18

RESULT 7

LOCUS BQ589768

DEFINITION E012680-024-020-D03-SP6 MP1Z-ADIS-024-storage root Beta vulgaris

CDNA clone 024-020-D03 5-PRIME, mRNA sequence.

ACCESSION BQ589768

VERSION BQ589768.1

KEYWORDS EST.

13 bp mRNA linear EST 06-DEC-2002


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/clone_lib="HNC (Human Normal Cartilage)"
/notes="vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

Query Match      0.4%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 5.4;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1130 CCTTCACCTCC 1140
Db 2 CCTTCACCTCC 12

RESULT 10
BG926067/c
LOCUS
DEFINITION HNC23-1-E8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION BG926067
VERSION BG926067.1 GI:14320590
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
TITLE Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteochondritic cartilage cDNA libraries
JOURNAL Osteoarthritis. Cartil. 9 (7), 641-653 (2001)
MEDLINE 21482651
PUBMED 11597177
COMMENT Contact: Sanjay Kumar
          GlaxoSmithKline
          709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
          Tel: 610-270-7245
          Fax: 610-270-5598
          Email: sanjay.kumar-1@gsk.com
          Seq primer: T7.
          Location/Qualifiers
          1..13
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          /mol_type="mRNA"
          /db_xref="taxon:9606"
          /tissue_type="cartilage"
          /lab_host="E.coli DH10 B"
          /clone_lib="HNC (Human Normal Cartilage)"
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          Directional"

Query Match      0.4%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 10;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1271 AGAAGTGGGAG 1281
Db 11 AGAAGGGGGAG 1

RESULT 11
BQ595423/c
LOCUS
DEFINITION E012693-024-022-N20-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
cDNA clone 024-022-N20 5-PRIME, mRNA sequence.
ACCESSION BQ595423
VERSION BQ595423.1 GI:26125006
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 13)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
          ADIS DNA core facility at MP1Z
          Max-Planck-Institute for Plant Breeding Research
          Carl-von-Linne Weg 10, 50829 Koeln, Germany
          Fax: 00492215062851
          Email: weisshaar@mpiz-koeln.mpg.de
          Insert Length: 13 Std Error: 0.00
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          Seq primer: SP6; CATACGATTAGGTGACACTATAG.
          Location/Qualifiers
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          /organism="Beta vulgaris"
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          /cultivar="KWS2320 (double haploid, monogerm breeding
          line)"
          /db_xref="GABI:191428"
          /db_xref="taxon:161934"
          /clone="024-022-N20"
          /tissue_type="developing root"
          /lab_host="EMDH10B"
          /clone_lib="MP1Z-ADIS-024-developing root"
          /note="vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
          cDNA library from sugar beet, library provided by KWS
          Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
          b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
          orientation:
          SP6-SalI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
          Sequencing granted in the context of the GABI-Beet
          project, local PI: Dr. Katharina Schneider, coordinator:
          Prof. Christian Jung; Sequence submission managed by
          RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.4%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 10;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 967 CGGTGGAATC 977
Db 13 CGGTGGAATTC 3

RESULT 12
CF307276
LOCUS
DEFINITION HDAL1--06-D23.g1 OsHDAC1-overexpressing transgenic rice lambda phage
cDNA library 1 (HDAL) Oryza sativa cDNA clone HDAL1--06-D23, mRNA
sequence.
ACCESSION CF307276
VERSION CF307276.1 GI:33679037
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 9)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,O.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source

1..9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="HDAL-06-D23"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDAC1-overexpressing transgenic rice lambda
phage cDNA library I (HDAL)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

Query Match 0.4%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1193 AGGTGGCAC 1201

Db 1 AGGTGGCAC 9

RESULT 13

CF307431

LOCUS

DEFINITION HDAL--06-K23.g1 OSHDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDAL) Oryza sativa cDNA clone HDAL--06-K23, mRNA

ACCESSION

CF307431

VERSION

CF307431.1

GI:33679192

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 9)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 321 6355

Fax: 82 31 321 6355

Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

Location/Qualifiers

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/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="HDAL-06-K23"

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/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli SOLR"

/clone_lib="OSHDAC1-overexpressing transgenic rice lambda

phage cDNA library I (HDAL)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

Query Match 0.4%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1193 AGGTGGCAC 1201

Db 1 AGGTGGCAC 9

RESULT 14

CF339065

LOCUS

DEFINITION RCL1--03-K22.g1 Regenerated callus lambda phage cDNA library (RCL1) Oryza sativa cDNA clone RCL1--03-K22, mRNA sequence.

ACCESSION

CF339065

VERSION

CF339065.1

GI:33826512

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 11)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 321 6355

Fax: 82 31 321 6355

Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

Location/Qualifiers

1..11

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="RCL1--03-K22"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli SOLR"

/clone_lib="Regenerated callus lambda phage cDNA library

(RCL1)"

/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:

XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'

end with SstI and 3' end with XhoI site. Callus was

induced on 2N6 media for 30 days and cultured for 36hrs on

regenerated media"

regenerated media"

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was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

Query Match 0.4%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1193 AGGTGGCAC 1201

Db 1 AGGTGGCAC 9

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CF339065/c

LOCUS

DEFINITION RCL1--03-K22.g1 Regenerated callus lambda phage cDNA library (RCL1) Oryza sativa cDNA clone RCL1--03-K22, mRNA sequence.

ACCESSION

CF339065

VERSION

CF339065.1

GI:33826512

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 11)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 321 6355

Fax: 82 31 321 6355

Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

Location/Qualifiers

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/organism="Oryza sativa"

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/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="RCL1--03-K22"

/tissue_type="callus"

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/lab_host="E.coli SOLR"

/clone_lib="Regenerated callus lambda phage cDNA library

(RCL1)"

/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:

XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'

end with SstI and 3' end with XhoI site. Callus was

induced on 2N6 media for 30 days and cultured for 36hrs on

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was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

Query Match 0.4%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1193 AGGTGGCAC 1201

Db 1 AGGTGGCAC 9

RESULT 15

CF339065/c

LOCUS

DEFINITION RCL1--03-K22.g1 Regenerated callus lambda phage cDNA library (RCL1) Oryza sativa cDNA clone RCL1--03-K22, mRNA sequence.

ACCESSION

CF339065

VERSION

CF339065.1

GI:33826512

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 11)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 321 6355

Fax: 82 31 321 6355

Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

Location/Qualifiers

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/clone_lib="Regenerated callus lambda phage cDNA library

(RCL1)"

/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:

XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'

end with SstI and 3' end with XhoI site. Callus was

induced on 2N6 media for 30 days and cultured for 36hrs on

regenerated media"

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was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

Query Match 0.4%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1193 AGGTGGCAC 1201

Db 1 AGGTGGCAC 9

RESULT 15

CF339065/c

LOCUS

DEFINITION RCL1--03-K22.g1 Regenerated callus lambda phage cDNA library (RCL1) Oryza sativa cDNA clone RCL1--03-K22, mRNA sequence.

ACCESSION

CF339065

VERSION

CF339065.1

GI:33826512

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 11)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University


```

SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 11)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice STs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES   Location/Qualifiers
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                /organism="Oryza sativa"
                /mol_type="mRNA"
                /cultivar="Nackdong"
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                /tissue_type="callus"
                /dev_stage="proliferated callus on 2N6 media for 30 days"
                /lab_host="E.coli: SOLR"
                /clone_lib="Regenerated callus lambda phage cDNA library
                (RCL1)"
                /notes="Vector: pBluescript SK(+); Site.1: SstI; Site.2:
                XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
                end with SstI and 3' end with XhoI site. Callus was
                induced on 2N6 media for 30 days and cultured for 36hrs on
                regenerated media"

Query Match      0.4%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 436 AAGTGCCAC 444
Db 11 AAGTGCCAC 3

RESULT 16
BQ585943
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DEFINITION E012531-024-014-K17-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
VERSION    BQ585943
KEYWORDS   EST.
SOURCE     Beta vulgaris
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 11)
AUTHORS    Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
TITLE      Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL    Plant J. 32 (5), 845-857 (2002)
MEDLINE    22362189
PUBMED     12472698
COMMENT    Contact: Weisshaar B
            ADIS DNA core facility at MP1Z
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weissaha@mpiz-koeln.mpg.de
            Insert Length: 11 Std Error: 0.00

SOURCE     Beta vulgaris
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 11)
AUTHORS    Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
TITLE      Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL    Plant J. 32 (5), 845-857 (2002)
MEDLINE    22362189
PUBMED     12472698
COMMENT    Contact: Weisshaar B
            ADIS DNA core facility at MP1Z
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weissaha@mpiz-koeln.mpg.de
            Insert Length: 11 Std Error: 0.00

FEATURES   Location/Qualifiers
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                line)"
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                /clone="024-014-K17"
                /tissue_type="leaf"
                /lab_host="EMDH10B"
                /clone_lib="MP1Z-ADIS-024-leaf"
                /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
                cDNA library from sugar beet, library provided by KWS
                Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
                b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
                orientation:
                SP6-Sali-CCACGGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
                Sequencing granted in the context of the GABI-Beet
                Project, local PI: Dr. Katharina Schneider, coordinator:
                Prof. Christian Jung; Sequence submission managed by
                RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match      0.4%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1519 GGACGGCGTG 1527
Db 2 GGACGGCGTG 10

RESULT 17
BQ593914
LOCUS      BQ593914
DEFINITION S015507-024-025-N20-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-025-N20 5-PRIME, mRNA sequence.
VERSION    BQ593914
KEYWORDS   EST.
SOURCE     Beta vulgaris
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 11)
AUTHORS    Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
TITLE      Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL    Plant J. 32 (5), 845-857 (2002)
MEDLINE    22362189
PUBMED     12472698
COMMENT    Contact: Weisshaar B
            ADIS DNA core facility at MP1Z
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weissaha@mpiz-koeln.mpg.de
            Insert Length: 11 Std Error: 0.00
            Plate: 25 row: N column: 20
            Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES   Location/Qualifiers
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                /organism="Beta vulgaris"
                /mol_type="mRNA"
                /cultivar="KWS2320 (double haploid, monogerm breeding
                line)"
                /db_xref="GABI:192937"
                /db_xref="taxon:161934"

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/clone="024-025-N20"
/tissue type="developing root"
/lab host="EMDH10B"
/notes="vector: pCMVSPORT6; Site 1: Sali; Site 2: Noti;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.4%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1519 GGACGCGTG 1527
Db 1 GGACGCGTG 9

RESULT 18
BQ592925/c
LOCUS
DEFINITION
BQ592925      12 bp      mRNA      linear      EST 06-DEC-2002
cDNA clone 024-028-F05-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
BQ592925
VERSION
KEYWORDS
SOURCE
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 12)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 28 row: F column: 05
Seq primer: SP6; CATACGATTAGTGACACTATAG.
Location/Qualifiers
1..12
/organism="Beta vulgaris"
/mol type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:193933"
/db_xref="taxon:161934"
/clone="024-028-F05"
/tissue type="developing root"
/lab host="EMDH10B"
/clone lib="MP1Z-ADIS-024-developing root"
/notes="vector: pCMVSPORT6; Site 1: Sali; Site 2: Noti;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.4%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1519 GGACGCGTG 1527
Db 11 GGACGCGTG 3

RESULT 19
BQ594497/c
LOCUS
DEFINITION
BQ594497      12 bp      mRNA      linear      EST 06-DEC-2002
cDNA clone 024-024-P14-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
BQ594497
VERSION
KEYWORDS
SOURCE
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 12)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 24 row: P column: 14
Seq primer: SP6; CATACGATTAGTGACACTATAG.
Location/Qualifiers
1..12
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/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:192358"
/db_xref="taxon:161934"
/clone="024-024-P14"
/tissue type="developing root"
/lab host="EMDH10B"
/clone lib="MP1Z-ADIS-024-developing root"
/notes="vector: pCMVSPORT6; Site 1: Sali; Site 2: Noti;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.4%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1519 GGACGCGTG 1527

```


and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
MEDLINE
PUBMED
COMMENT
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaa@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 28 row: F column: 05
Seq primer: SP6; CATACGATTAGTGACACTATAG.
Location/Qualifiers

FEATURES

source

1. .12
/organism="Beta vulgaris"
/mol_type="mRNA"
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/db_xref="GABI:193933"
/db_xref="taxon:161934"
/clone="024-F05"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MPiZ-ADIS-024-developing root"
/note="vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1238 CCTCGCGCTCCG 1249
||| ||| ||| |||
Db 1 CCCACGCGTCCG 12

RESULT 23
BQ594497
LOCUS
DEFINITION E012444-024-024-P14-SP6 MPiZ-ADIS-024-developing root Beta vulgaris
cDNA clone 024-024-P14 5-PRIME, mRNA sequence.
ACCESSION BQ594497
VERSION BQ594497.1 GI:26124080
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE E012444-024-024-P14-SP6 MPiZ-ADIS-024-developing root Beta vulgaris
cDNA clone 024-024-P14 5-PRIME, mRNA sequence.
AUTHORS Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
MEDLINE
PUBMED
COMMENT

ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Contact: Weishaar B
Fax: 00492215062851
Email: weishaa@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 28 row: F column: 05
Seq primer: SP6; CATACGATTAGTGACACTATAG.
Location/Qualifiers

Fax: 00492215062851
Email: weishaa@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 24 row: P column: 14
Seq primer: SP6; CATACGATTAGTGACACTATAG.
Location/Qualifiers

FEATURES

source

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line)"
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/db_xref="taxon:161934"
/clone="024-024-P14"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MPiZ-ADIS-024-developing root"
/note="vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1238 CCTCGCGCTCCG 1249
||| ||| ||| |||
Db 1 CCCACGCGTCCG 12

RESULT 24
BQ595544/c
LOCUS
DEFINITION E012691-024-022-A12-SP6 MPiZ-ADIS-024-developing root Beta vulgaris
cDNA clone 024-022-A12 5-PRIME, mRNA sequence.
ACCESSION BQ595544
VERSION BQ595544.1 GI:26125127
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE E012691-024-022-A12-SP6 MPiZ-ADIS-024-developing root Beta vulgaris
cDNA clone 024-022-A12 5-PRIME, mRNA sequence.
AUTHORS Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
MEDLINE
PUBMED
COMMENT

ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Contact: Weishaar B
Fax: 00492215062851
Email: weishaa@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 22 row: A column: 12
Seq primer: SP6; CATACGATTAGTGACACTATAG.
Location/Qualifiers

FEATURES

source

1. .12
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding

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line)"
/db_xref="GABI:191314"
/db_xref="taxon:161934"
/clone="024-022-A12"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGC-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1238 CCTCGCTCCG 1249
      ||| ||| |||
      12 CCCACGCGTCG 1

RESULT 25
CF282215
LOCUS
DEFINITION
14ETL--09-K01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
ORYZA SATIVA cDNA clone 14ETL--09-K01, mRNA sequence.
ACCESSION
CF282215
VERSION
CF282215.1 GI:33659602
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 12)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--09-K01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 752 GCACCTGCCATG 763

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Db 1 GCACCTGCCATG 12
      ||| ||| ||| |||
      13 bp mRNA linear EST 06-DEC-2002
      BQ589768
      E012680-024-020-D03-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
      cDNA clone 024-020-D03 5-PRIME, mRNA sequence.
      BQ589768
      ACCESSION
      BQ589768.1 GI:26119351
      KEYWORDS
      EST.
      SOURCE
      Beta vulgaris
      ORGANISM
      Beta vulgaris
      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
      Caryophyllales; Amaranthaceae; Beta.
      REFERENCE
      1 (bases 1 to 13)
      AUTHORS
      Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
      Drungewski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
      and Radelof,U.
      TITLE
      Construction of a 'unigene' cDNA clone set by oligonucleotide
      fingerprinting allows access to 25 000 potential sugar beet genes
      JOURNAL
      Plant J. 32 (5), 845-857 (2002)
      MEDLINE
      22362189
      PUBMED
      12472698
      COMMENT
      Contact: Weisshaar B
      ADIS DNA core facility at MP1Z
      Max-Planck-Institute for Plant Breeding Research
      Carl-von-Linne Weg 10, 50829 Koeln, Germany
      Fax: 00492215062851
      Email: weisshaar@piz-koeln.mpg.de
      Insert Length: 13 Std Error: 0.00
      Seq primer: 20 row: D column: 03
      Location/Qualifiers
      1..13
      /organism="Beta vulgaris"
      /mol_type="mRNA"
      /cultivar="KWS2320 (double haploid, monogerm breeding
      line)"
      /db_xref="GABI:190356"
      /db_xref="taxon:161934"
      /clone="024-020-D03"
      /tissue_type="storage root"
      /lab_host="EMDH10B"
      /clone_lib="MP1Z-ADIS-024-storage root"
      /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
      cDNA library from sugar beet, library provided by KWS
      Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
      b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
      orientation:
      SP6-Sali-CCACGCGTCGC-5prime-cDNA-polyA-CC-NotI-T7; Note:
      Sequencing granted in the context of the GABI-Beet
      Project, local PI: Dr. Katharina Schneider, coordinator:
      Prof. Christian Jung; Sequence submission managed by
      RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.4%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1014 TGAAGAGAGGG 1025
      ||| ||| ||| |||
      12 TCAAGAGAGGG 1

RESULT 27
BG926067
LOCUS
DEFINITION
HNC23-1-B9.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION
BG926067

```

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VERSION      BG926067.1  GI:14320590
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 13)
AUTHORS      Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
              Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
              Lark,M.W.
TITLE        Identification and initial characterization of 5000 expressed
              sequenced tags (ESTs) each from adult human normal and
              osteoarthritic cartilage cDNA libraries
JOURNAL      Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE      21482651
PUBMED       11597177
COMMENT      Contact: Sanjay Kumar
              UW2109
              GlaxoSmithKline
              709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
              Tel: 610-270-7245
              Fax: 610-270-5598
              Email: sanjay_kumar-1@gsk.com
              Seq primer: T7.
              Location/Qualifiers
FEATURES     source
              1..13
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /tissue_type="cartilage"
              /lab_host="E.coli DH10 B"
              /clone_lib="HNC (Human Normal Cartilage)"
              /notes="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
              Directional"
Query Match      0.4%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1126 TCCACCTTCACC 1137
Db 2 TCCCCCTTCTCC 13

RESULT 28
CF921234/C
LOCUS      gmhrw3-07_B06_1_046 Soybean root hair subtracted cDNA library
DEFINITION gmhrw3 Glycine max cDNA, mRNA sequence.
ACCESSION  CF921234
VERSION     CF921234.1  GI:38192028
KEYWORDS   EST.
SOURCE     Glycine max (soybean)
ORGANISM   Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 10)
Scheffler,B.E., Huang,S., Liu,X., Nguyen,H., Duke,M. and Stacey,G.
Expressed sequence tags from soybean root hair subtractive cDNA
library
Unpublished (2003)
Contact: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-4752
Fax: 573-882-0588
Email: stacey@missouri.edu
Single pass sequence
Seq primer: T7.
              Location/Qualifiers
FEATURES     source
              1..10
              /organism="Glycine max"
              /mol_type="mRNA"
              /db_xref="taxon:82"
              /tissue_type="root hairs"
              /clone_lib="Soybean root hair subtracted cDNA library
              gmhrw3"
              /notes="Organ: root hairs; Vector: pCE2-1 Topo; cDNA clones
              generated from soybean root hair tissue treated with
              Bradyrhizobium japonicum for 3 hours."

```

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/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="root hairs"
/clone_lib="Soybean root hair subtracted cDNA library
gmhrw3"
/notes="Organ: root hairs; Vector: pCE2-1 Topo; cDNA clones
generated from soybean root hair tissue treated with
Bradyrhizobium japonicum for 3 hours."
Query Match      0.4%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 5.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1179 GGCTCCCGC 1188
Db 10 GGATCCCGC 1

RESULT 29
CK298980
LOCUS      EST761694 Nicotiana benthamiana mixed tissue cDNA library,
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NEMDU48 3'
              end, mRNA sequence.
ACCESSION  CK298980
VERSION     CK298980.1  GI:39886896
KEYWORDS   EST.
SOURCE     Nicotiana benthamiana
ORGANISM   Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 10)
Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
Staskawicz,B., Jin,H. and Baker,B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other_ESTs: EST761693
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: GTA ATA CGA CTC ACT ATA GGG C.
              Location/Qualifiers
FEATURES     source
              1..10
              /organism="Nicotiana benthamiana"
              /mol_type="mRNA"
              /db_xref="taxon:4100"
              /clone="NEMDU48"
              /tissue_type="abiotic and biotic stress-treated leaves,
              callus tissue and root tissue"
              /lab_host="DH10B-Tona"
              /clone_lib="Nicotiana benthamiana mixed tissue cDNA
              library, normalized, full-length"
              /notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
              supplier: RNA was isolated from Nicotiana benthamiana
              tissues that include callus, roots from liquid culture
              grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
              cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
              challenged leaves (Pseudomonas syringae pv tomat 12 hr;
              Xanthomonas campestris pv campestris 12 hr, 18hr;
              Xanthomonas syringae pv phaseolicola 18hr, and Xanthomonas
              campestris pv vesicatoria 18hr). RNA was isolated from
              these tissues and pooled in approximately equal molar
              amounts."
Query Match      0.4%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 5.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1964 AGTTTTTTTT 1973
Db      1 ATTTTTTTTT 10

RESULT 30
BM395228/c
LOCUS   50072-2-8-B05.r.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM395228
VERSION 1
KEYWORDS
SOURCE  Tetrahymena thermophila
ORGANISM
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
1 (bases 1 to 11)
AUTHORS  Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE    EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL  Unpublished (2002)
COMMENT  Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..11
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
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/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK4; Details on library
Preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.4%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1211 AGGGGGCTGA 1220
Db      10 AGGGGGCAGA 1

RESULT 31
BQ590709/c
LOCUS   BQ590709
DEFINITION
E012597-024-018-024-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
cDNA clone 024-018-024 5-PRIME, mRNA sequence.
ACCESSION
BQ590709
VERSION 1
KEYWORDS
SOURCE  EST.
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 11)
AUTHORS  Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE    Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL  Plant J. 32 (5), 845-857 (2002)
MEDLINE  22362189
PUBMED   12472698
COMMENT  Contact: Weisshaar B

ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaa@mpiz-koeln.mpg.de
Insert Length: 11 Std Error: 0.00
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Seq primer: SP6; CATACGATTAGTGACACTATAG.
Location/Qualifiers
1..11
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/mol_type="mRNA"
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line)"
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/db_xref="taxon:161934"
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/tissue_type="storage root"
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/note="Vector: pCMVSPORT6; Site1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCAGCGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.4%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      976 TCCAAGCTCT 985
Db      10 TCCAAGCTCT 1

RESULT 32
BM395226/c
LOCUS   BM395226
DEFINITION
50072-2-8-B04.f.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM395226
VERSION 1
KEYWORDS
SOURCE  EST.
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
1 (bases 1 to 11)
AUTHORS  Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE    EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL  Unpublished (2002)
COMMENT  Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..11
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK4; Details on library
Preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.4%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1211 AGGGGGCTGA 1220
Db      10 AGGGGGCAGA 1

RESULT 31
BQ590709/c
LOCUS   BQ590709
DEFINITION
E012597-024-018-024-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
cDNA clone 024-018-024 5-PRIME, mRNA sequence.
ACCESSION
BQ590709
VERSION 1
KEYWORDS
SOURCE  EST.
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 11)
AUTHORS  Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE    Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL  Plant J. 32 (5), 845-857 (2002)
MEDLINE  22362189
PUBMED   12472698
COMMENT  Contact: Weisshaar B

```

preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.4%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 436 AAGTCCAC 445
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DB 11 AAGCCACA 2

RESULT 33
BQ587288/c
LOCUS
DEFINITION BQ587288 12 bp mRNA linear EST 06-DEC-2002
clone 024-010-G19-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA
ACCESSION BQ587288
VERSION BQ587288.1 GI:26116870
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE
AUTHORS BQ587288 12 bp mRNA linear EST 06-DEC-2002
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 12)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.

TITLE
JOURNAL Construction of a 'unigene' cDNA clone set by oligonucleotide
MEDLINE fingerprinting allows access to 25 000 potential sugar beet genes
PUBMED Plant J. 32 (5), 845-857 (2002)
COMMENT 22362189
12472698

CONTACT: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 10 row: G column: 19
Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES
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1..12
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/cultivar="KWS2320 (double haploid, monogerm breeding
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/clone="024-010-G19"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-leaf"
/note="Vector: PCWSPOR6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 808 TGTAGAAAA 817
||| |||||
DB 12 TGGAGAAAA 3

RESULT 35
BQ589761
LOCUS
DEFINITION BQ589761 12 bp mRNA linear EST 06-DEC-2002
cDNA clone 024-020-P03-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
ACCESSION BQ589761
VERSION BQ589761.1 GI:26119344
KEYWORDS EST.

RESULT 34
BQ587706/c
LOCUS
DEFINITION BQ587706 12 bp mRNA linear EST 06-DEC-2002
clone 024-010-G19-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA
ACCESSION BQ587706
VERSION BQ587706.1 GI:26117288
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE
AUTHORS BQ587706 12 bp mRNA linear EST 06-DEC-2002
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 12)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.

TITLE
JOURNAL Construction of a 'unigene' cDNA clone set by oligonucleotide
MEDLINE fingerprinting allows access to 25 000 potential sugar beet genes
PUBMED Plant J. 32 (5), 845-857 (2002)
COMMENT 22362189
12472698

CONTACT: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 10 row: G column: 19
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/tissue_type="leaf"
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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 808 TGTAGAAAA 817
||| |||||
DB 12 TGGAGAAAA 3

RESULT 35
BQ589761
LOCUS
DEFINITION BQ589761 12 bp mRNA linear EST 06-DEC-2002
cDNA clone 024-020-P03-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
ACCESSION BQ589761
VERSION BQ589761.1 GI:26119344
KEYWORDS EST.

SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 12)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
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/db_xref="GABI:190373"
/db_xref="taxon:161934"
/clone="024-020-P03"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPiZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
Query Match 0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1170 CAACTTTCGG 1179
Db 3 CTACTTTCGG 12
RESULT 36
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LOCUS BQ591624 12 bp mRNA linear EST 06-DEC-2002
DEFINITION cDNA clone 024-017-P07-SP6 MPiZ-ADIS-024-storage root Beta vulgaris
ACCESSION BQ591624
VERSION BQ591624.1 GI:26121207
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 12)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 17 row: P column: 07
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/clone="024-017-P07"
/tissue_type="storage root"
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/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
Query Match 0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1253 CCATCCCA 1262
Db 12 CCATCCCA 3
RESULT 37
AQ050979/c
LOCUS AQ050979 12 bp DNA linear GSS 24-MAR-1999
DEFINITION nbxb0004db1r CUGI Rice BAC Library Oryza sativa (japonica cultivar-group) genomic clone nbxb0004H22r, genomic survey sequence.
ACCESSION AQ050979
VERSION AQ050979.2 GI:4501770
KEYWORDS GSS.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Wing,R.A. and Dean,R.A.
TITLE A BAC End Sequencing Framework to Sequence the Rice Genome
JOURNAL Unpublished (1998)
COMMENT On Mar 23, 1999 this sequence version replaced gi:3325284.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCAATG
Class: BAC ends

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High quality sequence stop: 1.
FEATURES
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        /organism="Oryza sativa (japonica cultivar-group)"
        /mol_type="genomic DNA"
        /strain="Japonica"
        /cultivar="Nipponbare"
        /db_xref="taxon:39947"
        /clone="nxb0004H22r"
        /tissue type="Leaf"
        /lab host="E. coli DH10B"
        /clone_lib="CUGI Rice BAC Library"
        /notes="Vector: pBelOBAcl1; Site_1: HindIII; Site_2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
      Query Match          0.4%; Score 8.4; DB 1; Length 12;
      Best Local Similarity 90.0%; Pred. No. 22;
      Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1015 GAAAAAGAGG 1024
      |||||
Db      11 GAAAAATAGG 2

RESULT 38
B07312
LOCUS      B07312      12 bp      DNA      linear      GSS      26-MAR-1997
DEFINITION      G360T3 MVAT4 sheared genomic library Trypanosoma brucei rhodesiense
                genomic clone G360, genomic survey sequence.
ACCESSION      B07312.1      GI:1667053
VERSION      B07312.1
KEYWORDS      GSS.
SOURCE      Trypanosoma brucei rhodesiense
            Trypanosoma brucei rhodesiense
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE      1 (bases 1 to 12)
AUTHORS      El-Sayed,N.M.A. and Donelson,J.E.
TITLE      A survey of the Trypanosoma brucei rhodesiense genome using shotgun
            sequencing
JOURNAL      Mol. Biochem. Parasitol. 84 (2), 167-178 (1997)
MEDLINE      97237559
PUBMED      9084037
COMMENT      Other_GSSs: G360T7
            Contact: El-Sayed NMA
            John Donelson's Laboratory
            Howard Hughes Medical Institute
            300 EMRB, Dept. of Biochemistry, University of Iowa, Iowa City, IA
            52242
            Tel: 319 335 6918
            Fax: 319 335 6764
            Email: nelsayed@vaxa.weeg.uiowa.edu
            Insert Length: 700 Std Error: 200.00
            Seq primer: T3 primer
            Class: shotgun.
            Location/Qualifiers
FEATURES
  Query Match          0.4%; Score 8; DB 1; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1.3e+02;
  Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      955 TATCGCTACC 964
      |||||
Db      1 TATCGATACC 10

RESULT 39
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LOCUS      CF339091      8 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION      RCL1--03-M05. g1 Regenerated callus lambda phage cDNA library (RCL1)
                Oryza sativa cDNA clone RCL1--03-M05, mRNA sequence.
ACCESSION      CF339091.1      GI:33826564
VERSION      CF339091.1
KEYWORDS      EST.
SOURCE      Oryza sativa
            Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 8)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
            Location/Qualifiers
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      /organism="Oryza sativa"
      /mol_type="mRNA"
      /cultivar="Nackdong"
      /db_xref="taxon:4530"
      /clone="RCL1--03-M05"
      /tissue type="callus"
      /dev stage="proliferated callus on 2N6 media for 30 days"
      /lab host="E. coli SOLR"
      /clone_lib="Regenerated callus lambda phage cDNA library
            (RCL1)"
      /note="Vector: pBluescript SK(+); Site_1: SstI; Site_2:
            XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
            end with SstI and 3' end with XhoI site. Callus was
            induced on 2N6 media for 30 days and cultured for 36hrs on
            regenerated media"
  Query Match          0.4%; Score 8; DB 1; Length 8;
  Best Local Similarity 100.0%; Pred. No. 1.3e+02;
  Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      955 TATCGCTACC 964
      |||||
Db      1 TATCGATACC 10

RESULT 39
CF339091
LOCUS      CF339091      8 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION      RCL1--03-M05. g1 Regenerated callus lambda phage cDNA library (RCL1)
                Oryza sativa cDNA clone RCL1--03-M05, mRNA sequence.
ACCESSION      CF339091.1      GI:33826564
VERSION      CF339091.1
KEYWORDS      EST.
SOURCE      Oryza sativa
            Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 8)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
            Location/Qualifiers
FEATURES
  source
    1. .8
      /organism="Trypanosoma brucei rhodesiense"
      /mol_type="genomic DNA"
      /sub_species="rhodesiense"
      /db_xref="taxon:31286"
      /clone="G360"
      /dev stage="Bloodstream form"
      /clone_lib="MVAT4 sheared genomic library"
      /notes="Vector: PCR-Script Amp SK(+) (Stratagene); Site_1:
            Srf I; Genomic DNA was isolated from a cloned population
            of bloodstream trypanosomes reexpressing the MVAT4
            metacyclic variant surface glycoprotein (VSG). For the
            shotgun library construction, the DNA was mechanically
            sheared to give a tight size distribution, then
            blunt-ended, with T4 DNA polymerase. Following
            dephosphorylation with Shrimp Alkaline Phosphatase, DNA
            fragments were cloned into the PCR-Script vector
            (Stratagene)."
```

```

Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      301 CTGGAGCT 308
      1 CTGGAGCT 8

RESULT 40
CF277997
LOCUS      14ETL--03-L19.g1 Rice etiolated leaf plasmid cDNA library (14ETL) EST 14-AUG-2003
DEFINITION      Oryza sativa cDNA clone 14ETL--03-L19, mRNA sequence.
ACCESSION      CF277997.1 GI:33655383
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--03-L19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.4%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1966 TTTTITTT 1973
      1 TTTTITTT 8

RESULT 41
CF301888/c
LOCUS      7LEAF--06-O17.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza EST 15-AUG-2003
DEFINITION      sativa cDNA clone 7LEAF--06-O17, mRNA sequence.
ACCESSION      CF301888
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1966 TTTTITTT 1973
      1 TTTTITTT 8

RESULT 42
CF302851/c
LOCUS      7LEAF--08-M07.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza EST 15-AUG-2003
DEFINITION      sativa cDNA clone 7LEAF--08-M07, mRNA sequence.
ACCESSION      CF302851
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--03-L19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.4%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1966 TTTTITTT 1973
      1 TTTTITTT 8

RESULT 43
CF302851
LOCUS      7LEAF--08-M07.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza EST 15-AUG-2003
DEFINITION      sativa cDNA clone 7LEAF--08-M07, mRNA sequence.
ACCESSION      CF302851
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--06-O17"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.4%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1966 TTTTITTT 1973
      1 TTTTITTT 1
      8 TTTTITTT 1

```

```

TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="7LEAF--06-O17"
/tissue_type="leaf"
/dev_stage="7 days after germination"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.4%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1966 TTTTITTT 1973
      1 TTTTITTT 1
      8 TTTTITTT 1

RESULT 42
CF302851/c
LOCUS      7LEAF--08-M07.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza EST 15-AUG-2003
DEFINITION      sativa cDNA clone 7LEAF--08-M07, mRNA sequence.
ACCESSION      CF302851
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--08-M07"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.4%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1966 TTTTITTT 1973
      1 TTTTITTT 1
      8 TTTTITTT 1

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Query Match      0.4%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 TTTTTTTT 1973
DB 8 TTTTTTTT 1

RESULT 43
CF312818/c
LOCUS      8 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--08-L15.g1 ABF3-overexpressing transgenic rice plasmid cDNA
ACCESSION  CF312818
VERSION     CF312818.1 GI:33684579
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Ehrhartoideae; Magnoliophyta; Liliopsida; Poales; Poaceae;
Oryza.
1 (bases 1 to 8)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--08-L15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/cDNA_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      0.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 637 AGGAAGAA 644
DB 9 AGGAAGAA 2

RESULT 45
CF312817
LOCUS      9 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--08-L15.b1 ABF3-overexpressing transgenic rice plasmid cDNA
ACCESSION  CF312817
VERSION     CF312817.1 GI:33684578
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 9)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--08-L15"
/tissue_type="leaf"

Query Match      0.4%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 TTTTTTTT 1973
DB 8 TTTTTTTT 1

RESULT 44
CF309109/c
LOCUS      9 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--03-C20.b1 ABF3-overexpressing transgenic rice plasmid cDNA
ACCESSION  CF309109
VERSION     CF309109.1 GI:33680870
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

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/dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

Query Match 0.4%; Score 8; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1966 TTTTTTTT 1973
 |||||
 Db 1 TTTTTTTT 8

RESULT 46
 CF318771
 LOCUS
 DEFINITION HD--09-A13.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa CDNA clone HD--09-A13, mRNA sequence.

ACCESSION
 VERSION CF318771.1 GI:33690532
 KEYWORDS
 SOURCE EST.

ORGANISM
 Oryza sativa

Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 1 (bases 1 to 9)

AUTHORS
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE
 Large-scale Sequencing Analysis of Rice ESTs

COMMENT
 Unpublished (2003)

Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

source

1. .9
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="HD--09-A13"
 /tissue_type="callus"
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 /lab_host="E.coli DH10B"
 /clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.4%; Score 8; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1966 TTTTTTTT 1973
 |||||
 Db 1 TTTTTTTT 8

RESULT 47
 CF330649

LOCUS
 DEFINITION NACL--06-H06.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa CDNA clone NACL--06-H06, mRNA sequence.

ACCESSION
 VERSION CF330649

KEYWORDS
 SOURCE EST.

ORGANISM
 Oryza sativa

Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 1 (bases 1 to 9)

AUTHORS
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE
 Large-scale Sequencing Analysis of Rice ESTs

JOURNAL
 COMMENT Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

source

1. .9
 /organism="Oryza sativa"
 /mol_type="mRNA"
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 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.4%; Score 8; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1966 TTTTTTTT 1973
 |||||
 Db 1 TTTTTTTT 8

RESULT 48

CF333615

LOCUS

DEFINITION

library (JMT) Oryza sativa CDNA clone JMT--02-J09, mRNA sequence.

ACCESSION

VERSION CF333615.1 GI:33815525

KEYWORDS

SOURCE EST.

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

JOURNAL

COMMENT Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

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source
1. .10
/organism="Oryza sativa"
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/cultivar="Nackdong"
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/clone="JMT--02-J09"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      0.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1309 GACACTGA 1316
Db 2 GACACTGA 9

RESULT 49
CA794390/c
LOCUS
DEFINITION
CA794390 10 bp mRNA linear EST 05-DEC-2002
Theobroma cacao Cac BL 1340 (Bean and Leaf from Amelonardo type Cacao)
CA794390
VERSION
KEYWORDS
SOURCE
ORGANISM
Theobroma cacao (cacao)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
Theobroma.
1 (bases 1 to 10)
Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,
Retzel, E.R. and Jones, C.A.
Gene discovery and microarray analysis of cacao (Theobroma cacao
L.) varieties
Planta 216 (2), 255-264 (2002)
22337596
MEDLINE
PUBMED
12447539
COMMENT
Contact: Jones, Paul
Masterfoods
3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
Tel: +44 1664 416644
Email: Paul.Jones@eu.affem.com
Seq primer: T3.
FEATURES
Location/Qualifiers
1. .10
/organism="Theobroma cacao"
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/clone="Cac BL 1340"
/tissue_type="Mature leaf and mature bean"
/cell_type="Whole organ"
/dev_stage="maturity"
/lab_host="XL-1 Blue MRF"
/clone_lib="Cac BL (Bean and Leaf from Amelonardo type
Cacao)"
/note="Vector: pBK-CMV; Bean and leaf tissue from an
Amelonado type Cacao tree."

Query Match      0.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 183 GGAAGCCC 190
Db 8 GGAAGCCC 1

RESULT 50
CF322692/c
LOCUS
DEFINITION
CF322692 11 bp mRNA linear EST 18-AUG-2003
HDN--01-M19_g1 OshDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa CDNA clone HDN--01-M19, mRNA
sequence.
ACCESSION
CF322692
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 11)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
Location/Qualifiers
1. .11
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDN--01-M19"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OshDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1236 AGCCCTCG 1243
Db 11 AGCCCTCG 4

RESULT 51
BG925521/c
LOCUS
DEFINITION
BG925521 12 bp mRNA linear EST 06-NOV-2001
HNC5-1-D3.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION
BG925521
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 12)
Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,
Sathie, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and

```

Lark.M.W.
 Identification and initial characterization of 5000 expressed
 sequenced tags (ESTs) each from adult human normal and
 osteoarthritic cartilage cDNA libraries
 Osteoarthr. Cartil. 9 (7), 641-653 (2001)
 21482651
 MEDLINE
 PUBMED
 COMMENT
 Contact: Sanjay Kumar
 UW2109
 GlaxoSmithKline
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
 Tel: 610-270-7245
 Fax: 610-270-5598
 Email: sanjay.kumar-legsk.com
 Seq primer: T7.

FEATURES

Location/Qualifiers
 1..12
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="cartilage"
 /lab_host="E.coli DH10 B"
 /clone_lib="HMC (Human Normal Cartilage)"
 /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
 Directional"

Query Match 0.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 78 GGAGGGGA 85
 |||||
 Db 12 GGAGGGGA 5
 RESULT 52
 BQ587288
 LOCUS
 DEFINITION
 clone 024-010-G19-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA
 VERSION
 BQ587288.1 GI:26116870
 KEYWORDS
 EST.
 SOURCE
 Beta vulgaris
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 12)
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)
 Plant J. 32 (5), 845-857 (2002)
 MEDLINE
 PUBMED
 COMMENT
 Contact: Weishaar B
 ADIS DNA core facility at MPIZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert Length: 12 Std Error: 0.00
 Plate: 10 row: G column: 19
 Seq primer: SP6; CATACGATTAGTGACACTAG.

FEATURES

Location/Qualifiers
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 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding
 line)"
 /db_xref="GABI:185570"

/db_xref="taxon:161934"
 /clone="024-010-G19"
 /tissue_type="leaf"
 /lab_host="EMDH10B"
 /clone_lib="MPIZ-ADIS-024-leaf"
 /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCAGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1683 TTTTCTCT 1690
 |||||
 Db 1 TTTTCTCT 8

RESULT 53

BQ587706
 LOCUS
 DEFINITION
 E012340-024-010-G19-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
 024-010-G19 5-PRIME, mRNA sequence.
 VERSION
 BQ587706.1 GI:26117288
 KEYWORDS
 EST.
 SOURCE
 Beta vulgaris
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 12)
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)
 Plant J. 32 (5), 845-857 (2002)
 MEDLINE
 PUBMED
 COMMENT
 Contact: Weishaar B
 ADIS DNA core facility at MPIZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert Length: 12 Std Error: 0.00
 Plate: 10 row: G column: 19
 Seq primer: SP6; CATACGATTAGTGACACTAG.

FEATURES

Location/Qualifiers
 1..12
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 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding
 line)"
 /db_xref="GABI:185160"
 /db_xref="taxon:161934"
 /clone="024-010-G19"
 /tissue_type="leaf"
 /lab_host="EMDH10B"
 /clone_lib="MPIZ-ADIS-024-leaf"
 /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:

```

SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match      0.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1683 TTTTCTCT 1690
Db 1 TTTTCTCT 8

RESULT 54
BQ595423
LOCUS
DEFINITION      BQ595423      13 bp mRNA linear EST 06-DEC-2002
                  cDNA clone 024-022-N20-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
ACCESSION      BQ595423.1 GI:26125006
VERSION
KEYWORDS
SOURCE
ORGANISM      Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 13)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE      Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
MEDLINE
PUBMED
COMMENT      Contact: Weisshaar B
                  ADIS DNA core facility at MP1Z
                  Max-Planck-Institute for Plant Breeding Research
                  Carl-von-Linne Weg 10, 50829 Koeln, Germany
                  Fax: 00492215062851
                  Email: weisshaar@mpiz-koeln.mpg.de
                  Insert Length: 13 Std Error: 0.00
                  Plate: 22 row: N column: 20
Seq primer: SP6; CATACGATTTAGTGACACTATAG.
Location/Qualifiers
1. 13
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/mol type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:191428"
/db_xref="taxon:161934"
/clone="024-022-N20"
/tissue type="developing root"
/lab host="EMPH108"
/clone lib="MP1Z-ADIS-024-developing root"
/note="vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Binbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.4%; Score 8; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 50 GAGAAATTC 57
Db 1 GAGAAATTC 8

RESULT 55
BQ927412
LOCUS
DEFINITION      BQ927412      11 bp mRNA linear EST 06-NOV-2001
                  HNC1-1-G11.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
ACCESSION      BQ927412.1 GI:14321935
VERSION
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 11)
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
TITLE      Identification and initial characterization of 5000 expressed
sequence tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
JOURNAL
MEDLINE
PUBMED
COMMENT      Contact: Sanjay Kumar
                  GlaxoSmithKline
                  709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
                  Tel: 610-270-7245
                  Fax: 610-270-5598
                  Email: sanjay_kumar-legsk.com
Seq primer: F7.
Location/Qualifiers
1. 11
/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/tissue type="cartilage"
/lab host="E.coli DH10 B"
/clone lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site 1: Sali; Site 2: NotI;
Directional"

Query Match      0.4%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 841 CTACCCCGAGAT 851
Db 1 CTACGCCAGCT 11

RESULT 56
BQ927896/c
LOCUS
DEFINITION      BQ927896      11 bp mRNA linear EST 06-NOV-2001
                  HNC45-1-D11.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
ACCESSION      BQ927896
VERSION
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 11)
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
TITLE      Identification and initial characterization of 5000 expressed
sequence tags (ESTs) each from adult human normal and

```



```

JOURNAL Osteoarthritic cartilage cDNA libraries
MEDLINE Osteoarthr. Cartil. 9 (7), 641-653 (2001)
PUBMED 21482651
COMMENT 11597177
Contact: Sanjay Kumar
UW2109 GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@gsk.com
Seq primer: 17
          ||| ||| |||
          1 GTGGCGCCGA 11

FEATURES
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/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.Coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI; Directional"

Query Match 0.4%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1011 ACCTGAAAAAG 1021
Db ||||| |||
11 ACCTGCAACG 1

RESULT 57
BM395997
LOCUS 11 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-15-D12.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM395997
VERSION BM395997.1 GI:18196050
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 11)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
          ||| ||| |||
          1..11
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.4%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 877 TCAGGCACAC 887
Db ||||| |||
11 TCCGGCGCCAC 1

RESULT 59
BM395997
LOCUS 11 bp mRNA linear EST 06-DRC-2002
DEFINITION 5009-0-15-D12.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM395997
VERSION BM395997.1 GI:18196050
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 11)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
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          1..11
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/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.4%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1359 GTTGGCGTGA 1369

```

Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaa@piz-koeln.mpg.de
 Insert Length: 11 Std Error: 0.00
 Plate: 14 row: K column: 17
 Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES

source
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 /db_xref="GABI:196918"
 /db_xref="taxon:161934"
 /clone="024-014-K17"
 /tissue_type="leaf"
 /lab_host="EMDH10B"
 /clone_lib="MP12-ADIS-024-leaf"
 /note="Vector: PCWSPOR76; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinzellener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
 SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.4%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 26;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1239 CCTCGCGTCG 1249

Db 11 CCACGCGTCG 1

RESULT 60

BQ593914/c
 LOCUS
 DEFINITION S015507-024-025-N20-SP6 MP12-ADIS-024-developing root Beta vulgaris
 cDNA clone 024-025-N20 5-PRIME, mRNA sequence.
 ACCESSION BQ593914
 VERSION BQ593914.1 GI:26123497
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE

AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL

MEDLINE Plant J. 32 (5), 845-857 (2002)
 PUBMED 12472698

COMMENT

Contact: Weishaar B
 ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851

FEATURES

source
 1. .11
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /db_xref="taxon:161934"
 /clone="024-014-K17"
 /tissue_type="leaf, stem"
 /dev_stage="1-month seedlings - 1 cm tall - 8 leaf"
 /clone_lib="Dso1-AAFC-ECORC_cold_stressed_Flixweed_seedling"
 /note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: Eco RI; Site 2: Xho I; Plants were grown for 1 month at 20°C/16 hrs light/day (average 8 leaves, 1 cm tall, weight 0.02g/plant). Then they were exposed to 20°C, 12 hrs light/day, for 1 week. Library prepared by C. Piche using Stratagene kit."

/mol_type="mRNA"
 /cultiivar="KWS2320 (double haploid, monogerm breeding line)"
 /db_xref="GABI:192937"
 /db_xref="taxon:161934"
 /clone="024-025-N20"
 /tissue_type="developing root"
 /lab_host="EMDH10B"
 /clone_lib="MP12-ADIS-024-developing root"
 /note="Vector: PCWSPOR76; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinzellener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
 SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.4%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 26;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1238 CCTCGCGTCG 1248

Db 11 CCCACGCGTCG 1

RESULT 61

BQ238234
 LOCUS
 DEFINITION Ds01_01e11 R Ds01-AAFC-ECORC cold stressed Flixweed seedlings
 Descurainia sophia cDNA clone Ds01_01e11, mRNA sequence.
 ACCESSION BQ238234
 VERSION BQ238234.1 GI:22750059
 KEYWORDS EST.
 SOURCE Descurainia sophia
 ORGANISM Descurainia sophia
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Descurainia.

REFERENCE

AUTHORS Singh,J.A., Piche,C., Couroux,P., De Moors,A., Harris,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Spott,D. and Tinker,N.A.
 Expressed Sequence Tags from Cold-Stressed Descurainia sophia Seedlings

JOURNAL

COMMENT Unpublished (2001)
 Contact: Singh,J.A.
 Eastern Cereal and Oilseed Research Centre
 Agriculture and Agri-food Canada
 KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KIA 0C6, Canada

FEATURES

source
 1. .11
 /organism="Descurainia sophia"
 /mol_type="mRNA"
 /db_xref="taxon:89411"
 /clone="Ds01_01e11"
 /tissue_type="leaf, stem"
 /dev_stage="1-month seedlings - 1 cm tall - 8 leaf"
 /clone_lib="Ds01-AAFC-ECORC_cold_stressed_Flixweed_seedling"
 /note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: Eco RI; Site 2: Xho I; Plants were grown for 1 month at 20°C/16 hrs light/day (average 8 leaves, 1 cm tall, weight 0.02g/plant). Then they were exposed to 20°C, 12 hrs light/day, for 1 week. Library prepared by C. Piche using Stratagene kit."

Query Match 0.4%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 26;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 371 AGAGAGATAGT 381
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 Db 1 AGAGAACTAGT 11

RESULT 62
 CF323154 11 bp mRNA linear EST 18-AUG-2003
 LOCUS HDN-03-B04.g1 OshDAC1-overexpressing transgenic rice lambda phage
 DEFINITION cDNA library II (HDN) Oryza sativa cDNA clone HDN-03-B04, mRNA
 sequence.

ACCESSION CF323154
 VERSION CF323154.1 GI:33794534
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 11)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

TITLE Contact: Nahm B.H.
 JOURNAL Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 COMMENT of Bioscience and Bioinformatics, Myongji University
 Yongsin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhah@gbio.com, bnhah@bio.myongji.ac.kr.

FEATURES
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 1..11
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 /cultivar="Nackdong"
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 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
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 phage cDNA library II (HDN)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
 5' end with EcoRI and 3' end with XhoI site. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.4%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 26;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 827 GCACGAGGTG 837
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 Db 1 GCACGAGGGTG 11

RESULT 63
 CF543031/c 11 bp mRNA linear EST 22-SEP-2003
 LOCUS S01532-024-030-P02-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
 DEFINITION 024-030-P02 5-PRIME, mRNA sequence.

ACCESSION CF543031
 VERSION CF543031.1 GI:34891471
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 11)
 Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
 Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lebrach, H.
 and Radelof, U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)

JOURNAL 22362189
 MEDLINE 12472698
 PUBMED
 COMMENT Contact: Weisshaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaa@mpiz-koeln.mpg.de
 Insert Length: 11 Std Error: 0.00
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 Seq primer: SP6.

FEATURES
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 /db_xref="GABI:936732"
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 /lab_host="EMPH10B"
 /clone_lib="MP1Z-ADIS-024-leaf"
 /note="Vector: PCMVSPOR16; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-SalI-CCACGCGCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.4%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 26;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1092 CACCCCCCACC 1102
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 Db 11 CCCCCCCCCC 1

RESULT 64
 BQ587870/c 12 bp mRNA linear EST 06-DEC-2002
 LOCUS S013708-024-009-P23-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
 DEFINITION 024-009-P23 5-PRIME, mRNA sequence.

ACCESSION BQ587870
 VERSION BQ587870.1 GI:26117452
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 12)
 Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
 Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lebrach, H.
 and Radelof, U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)

JOURNAL 22362189
 MEDLINE

```

PUBMED 12472698
COMMENT Contact: Weishaar B
        ADIS DNA core facility at MPIZ
        Max-Planck-Institute for Plant Breeding Research
        Carl-von-Linne Weg 10, 50829 Koeln, Germany
        Fax: 00492215062851
        Email: weishaa@mpiz-koeln.mpg.de
        Insert Length: 12 Std Error: 0.00
        Plate: 9 row: P column: 23
        Seq primer: SP6; CATACGATTAGGTGACACTATAG.
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        Location/Qualifiers
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            line)"
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            /db_xref="taxon:161934"
            /clone="024-009-P23"
            /tissue_type="leaf"
            /lab_host="EMDH10B"
            /clone_lib="MPIZ-ADIS-024-leaf"
            /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
            cDNA library from sugar beet, library provided by KWS
            Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
            b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
            orientation:
            SP6-Sali-CCACGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
            Sequencing granted in the context of the GABI-Beet
            project, local PI: Dr. Katharina Schneider, coordinator:
            Prof. Christian Jung; Sequence submission managed by
            RZPD/GABI-Primary database: http://gabi.rzpd.de"
            Query Match 0.4%; Score 7.8; DB 1; Length 12;
            Best Local Similarity 81.8%; Pred. No. 45;
            Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 133 TCACGTCTCAC 143
Db 11 TCGACTGCCAC 1
RESULT 65
BQ589761/c
LOCUS BQ589761 12 bp mRNA linear EST 06-DEC-2002
DEFINITION BQ12680-024-020-P03-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-020-P03 5-PRIME, mRNA sequence.
ACCESSION BQ589761
VERSION BQ589761.1 GI:26119344
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 12)
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
REFERENCE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerpringing allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL 22362189
MEDLINE 12472698
PUBMED
COMMENT Contact: Weishaar B
        ADIS DNA core facility at MPIZ
        Max-Planck-Institute for Plant Breeding Research
        Carl-von-Linne Weg 10, 50829 Koeln, Germany
        Fax: 00492215062851
        Email: weishaa@mpiz-koeln.mpg.de
        Insert Length: 12 Std Error: 0.00
        Plate: 20 row: P column: 03
        Seq primer: SP6; CATACGATTAGGTGACACTATAG.
FEATURES
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            /cultivar="KWS2320 (double haploid, monogerm breeding
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            /db_xref="GABI:184996"
            /db_xref="taxon:161934"
            /clone="024-009-P23"
            /tissue_type="leaf"
            /lab_host="EMDH10B"
            /clone_lib="MPIZ-ADIS-024-leaf"
            /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
            cDNA library from sugar beet, library provided by KWS
            Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
            b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
            orientation:
            SP6-Sali-CCACGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
            Sequencing granted in the context of the GABI-Beet
            project, local PI: Dr. Katharina Schneider, coordinator:
            Prof. Christian Jung; Sequence submission managed by
            RZPD/GABI-Primary database: http://gabi.rzpd.de"
            Query Match 0.4%; Score 7.8; DB 1; Length 12;
            Best Local Similarity 81.8%; Pred. No. 45;
            Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 605 GCACATGGAC 615
Db 11 GCAAGTAGAC 1
RESULT 66
BQ7312/c
LOCUS BQ7312 12 bp DNA linear GSS 26-MAR-1997
DEFINITION BQ360T3 MVAT4 sheared genomic library trypanosoma brucei rhodesiense
genomic clone G360, genomic survey sequence.
ACCESSION BQ7312
VERSION BQ7312.1 GI:1667053
KEYWORDS GSS.
SOURCE Trypanosoma brucei rhodesiense
ORGANISM Trypanosoma brucei rhodesiense
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 12)
El-Sayed,N.M.A. and Donelson,J.E.
REFERENCE A survey of the Trypanosoma brucei rhodesiense genome using shotgun
sequencing
Mol. Biochem. Parasitol. 84 (2), 167-178 (1997)
JOURNAL 97237559
MEDLINE 9084037
PUBMED
COMMENT Other_GSSs: G360T7
Contact: El-Sayed NMA
John Donelson's Laboratory
Howard Hughes Medical Institute
300 EMBR, Dept. of Biochemistry, University of Iowa, Iowa City, IA
52242
Tel: 319 335 6918
Fax: 319 335 6764
Email: nelsayed@vaxa.weeg.uiowa.edu
Insert Length: 700 Std Error: 200.00
Seq primer: T3 primer
Class: shotgun.
FEATURES
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            1..12
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            /clone="G360"
            /dev_stage="Bloodstream form"
            /clone_lib="MVAT4 sheared genomic library"
            /note="Vector: PCR-Script Amp SK(+)(Stratagene); Site_1:

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Srf I; Genomic DNA was isolated from a cloned population of bloodstream trypanosomes reexpressing the MVAT4 metacyclic variant surface glycoprotein (VSG). For the shotgun library construction, the DNA was mechanically sheared to give a tight size distribution, then blunt-ended with T4 DNA polymerase. Following dephosphorylation with Shrimp Alkaline Phosphatase, DNA fragments were cloned into the PCR-Script vector (Stratagene)."

Query Match 0.4%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1403 ACAGATCGAT 1413
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Db 12 ACGGATCGAT 2

RESULT 67
CNS06E5N/c
LOCUS
DEFINITION CNS06E5N 9 bp DNA linear GSS 17-JUN-2001
T3 end of clone AROAA018H04 of library AROAA from strain CBS 732 of Zygosaccharomyces rouxii, genomic survey sequence.
ACCESSION
VERSION AL394689
KEYWORDS
SOURCE AL394689.1 GI:12145788
ORGANISM
Zygosaccharomyces rouxii
Zygosaccharomyces rouxii
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.
REFERENCE
1 (bases 1 to 9)
Souciet, J.-L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Liorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekai, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
JOURNAL

Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
FEMS Lett. 487 (1), 3-12 (2000)
11152876
2 (bases 1 to 9)
de Montigny, J., Straub, M., Potier, S., Tekai, F., Dujon, B., Wincker, P., Artiguenave, F. and Souciet, J.
Genomic exploration of the hemiascomycetous yeasts: 8.
Zygosaccharomyces rouxii
FEMS Lett. 487 (1), 52-55 (2000)
11152883
3 (bases 1 to 9)
Genoscope.
Direct Submission
Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES
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/mol_type="genomic DNA"
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/db_xref="taxon:4956"

/clone="AROAA018H04"
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/note="end : 13"

Query Match 0.4%; Score 7.6; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 904 GTCAATTTT 911
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Db 9 GTCAATTTT 2

RESULT 68
CF307276/c
LOCUS
DEFINITION CF307276 9 bp mRNA linear EST 15-AUG-2003
HDAL1-06-D23.g1 OSHDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDAL1) Oryza sativa cDNA clone HDAL1-06-D23, mRNA sequence.
ACCESSION
VERSION CF307276.1 GI:33679037
KEYWORDS
SOURCE Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 9)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnab@bio.com, bnhnab@bio.myongji.ac.kr.

FEATURES
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1. .9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/lab_host="E.coli SOLR"
/clone_lib="OSHDA1-overexpressing transgenic rice lambda phage cDNA library I (HDAL1)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1124 GTTCCACCT 1132
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Db 9 GTTCCACCT 1

RESULT 69
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LOCUS
DEFINITION CF307431 9 bp mRNA linear EST 15-AUG-2003
HDAL1-06-K23.g1 OSHDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDAL1) Oryza sativa cDNA clone HDAL1-06-K23, mRNA sequence.
ACCESSION
VERSION CF307431.1 GI:33679037
KEYWORDS
SOURCE Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 9)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnab@bio.com, bnhnab@bio.myongji.ac.kr.

FEATURES
source
1. .9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="HDAL1-06-D23"
/tissue_type="callus"
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/lab_host="E.coli SOLR"
/clone_lib="OSHDA1-overexpressing transgenic rice lambda phage cDNA library I (HDAL1)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1124 GTTCCACCT 1132
||| |||||
Db 9 GTTCCACCT 1

RESULT 69
CF307431/c
LOCUS
DEFINITION CF307431 9 bp mRNA linear EST 15-AUG-2003
HDAL1-06-K23.g1 OSHDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDAL1) Oryza sativa cDNA clone HDAL1-06-K23, mRNA sequence.
ACCESSION
VERSION CF307431.1 GI:33679037
KEYWORDS
SOURCE Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 9)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnab@bio.com, bnhnab@bio.myongji.ac.kr.

FEATURES
source
1. .9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDAL1-06-D23"
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/lab_host="E.coli SOLR"
/clone_lib="OSHDA1-overexpressing transgenic rice lambda phage cDNA library I (HDAL1)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1124 GTTCCACCT 1132
||| |||||
Db 9 GTTCCACCT 1

RESULT 69
CF307431/c
LOCUS
DEFINITION CF307431 9 bp mRNA linear EST 15-AUG-2003
HDAL1-06-K23.g1 OSHDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDAL1) Oryza sativa cDNA clone HDAL1-06-K23, mRNA sequence.
ACCESSION
VERSION CF307431.1 GI:33679037
KEYWORDS
SOURCE Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 9)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnab@bio.com, bnhnab@bio.myongji.ac.kr.

FEATURES
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1. .9
/organism="Oryza sativa"
/mol_type="mRNA"
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/db_xref="taxon:4530"
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/tissue_type="callus"
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/lab_host="E.coli SOLR"
/clone_lib="OSHDA1-overexpressing transgenic rice lambda phage cDNA library I (HDAL1)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1124 GTTCCACCT 1132
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Db 9 GTTCCACCT 1

RESULT 69
CF307431/c
LOCUS
DEFINITION CF307431 9 bp mRNA linear EST 15-AUG-2003
HDAL1-06-K23.g1 OSHDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDAL1) Oryza sativa cDNA clone HDAL1-06-K23, mRNA sequence.
ACCESSION
VERSION CF307431.1 GI:33679037
KEYWORDS
SOURCE Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 9)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnab@bio.com, bnhnab@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDA1-overexpressing transgenic rice lambda phage cDNA library I (HDAL1)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

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VERSION CF307431.1 GI:33679192
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 9)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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        /clone_lib="OshDAC1-overexpressing transgenic rice lambda
        phage cDNA library I (HDAL)"
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        XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
        was inserted into lambda Uni-ZAP XR vector at 5' end with
        EcoRI and 3' end with XhoI site. mRNA was derived from
        rice Histone Deacetylase overexpression line."
    Query Match 0.3%; Score 7.4; DB 1; Length 9;
    Best Local Similarity 88.9%; Pred. No. 1.1e+02;
    Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1124 GTTCCACCT 1132
Db 9 GTGCCACCT 1

RESULT 70
CA850813
LOCUS D06G10_G10_14.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
DEFINITION cDNA clone D06G10 5', mRNA sequence.
ACCESSION CA850813
VERSION CA850813.1 GI:33387606
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 9)
AUTHORS Alkharouf,N.W., Khan,R. and Matthews,B.F.
TITLE Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
JOURNAL Unpublished (2002)
COMMENT Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ba.ars.usda.gov.

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FEATURES
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        /dev_stage="Seedlings"
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        extracted from Peking roots 2 and 4 days past invasion."
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    Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 992 TTGTTTGTG 1000
Db 1 TTGTTTATG 9

RESULT 71
CF313414
LOCUS HD--01-I15.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--01-I15, mRNA sequence.
ACCESSION CF313414
VERSION CF313414.1 GI:33685175
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 9)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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        /db_xref="taxon:4530"
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        /tissue_type="callus"
        /dev_stage="proliferated callus on 2N6 media for 2 weeks"
        /lab_host="E.coli DH10B"
        /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
        cDNA library (HD)"
        /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
        treated with ABA(20um) for 1hr. Oligo-capped mRNA was
        reverse transcribed and then used for PCR. mRNA was
        derived from rice Histone Deacetylase overexpression
        line."
    Query Match 0.3%; Score 7.4; DB 1; Length 9;
    Best Local Similarity 88.9%; Pred. No. 1.1e+02;
    Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 817 AGCCTGGAG 825
Db 1 AGACTGGAG 9

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RESULT 72
CF313414/c
LOCUS
DEFINITION HD--01-I15.bi OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--01-I15, mRNA sequence.

ACCESSION CF313414
VERSION CF313414.1 GI:33685175
KEYWORDS EST.
SOURCE Oryza sativa

ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 9)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
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/organism="Oryza sativa"
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/db_xref="taxon:4530"
/clone="HD--01-I15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN)"
/note="Vector: pCR4-TOPO; Site:1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 CTCACGCT 1090
Db 9 CTCACGCT 1

RESULT 73
CF323490
LOCUS
DEFINITION HDN--03-P21.g1 OSHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa cDNA clone HDN--03-P21, mRNA sequence.

ACCESSION CF323490
VERSION CF323490.1 GI:33795236
KEYWORDS EST.
SOURCE Oryza sativa

ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 9)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Query Match 0.3%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 CTCACGCT 1090
Db 9 CTCACGCT 1

RESULT 73
CF323490
LOCUS
DEFINITION HDN--03-P21.g1 OSHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa cDNA clone HDN--03-P21, mRNA sequence.

ACCESSION CF323490
VERSION CF323490.1 GI:33795236
KEYWORDS EST.
SOURCE Oryza sativa

ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 9)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..9
/organism="Oryza sativa"
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/cultivar="Nackdong"
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/clone_lib="OSHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN)"
/note="Vector: pBluescript SK(+); Site:1: EcoRI; Site:2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 827 GCACGAGT 835

Db 1 GCACGAGT 9

RESULT 74

CF307092

LOCUS

DEFINITION

HD1--05-L14.g1 OSHDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDA1) Oryza sativa cDNA clone HDA1--05-L14, mRNA sequence.

ACCESSION

CF307092

VERSION

CF307092.1

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 9)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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/lab_host="E.coli SOIR"
/clone_lib="OSHDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDA1)"
/note="Vector: pBluescript SK(+); Site:1: EcoRI; Site:2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA

was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1524 CGTGCTCG 1532
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Db 1 CGAGCTCG 9

RESULT 75
CF322585
LOCUS
DEFINITION HDN--01-H22.g1 OshDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa cDNA clone HDN--01-H22, mRNA sequence.
ACCESSION CF322585
VERSION CF322585.1 GI:33793411
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 9)
REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1443 GCGCGAGGC 1451
||| |||||
Db 1 GCACGAGGC 9

RESULT 76
CF322585/c
LOCUS
DEFINITION HDN--01-H22.g1 OshDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa cDNA clone HDN--01-H22, mRNA sequence.
ACCESSION CF322585

Query Match 0.3%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1524 CGTGCTCG 1532
||| |||||
Db 1 CGAGCTCG 9

RESULT 75
CF322585
LOCUS
DEFINITION HDN--01-H22.g1 OshDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa cDNA clone HDN--01-H22, mRNA sequence.
ACCESSION CF322585

VERSION CF322585.1 GI:33793411
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 9)
REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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/clone="HDN--01-H22"
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/lab_host="E.coli SOLR"
/clone_lib="OshDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1877 GCCTCATGC 1885
|||||
Db 9 GCCTCATGC 1

RESULT 77
CF325534
LOCUS
DEFINITION JMT1--03-H24.g1 AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1) Oryza sativa cDNA clone JMT1--03-H24, mRNA sequence.
ACCESSION CF325534
VERSION CF325534.1 GI:33799350
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 9)
REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers


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1. .9
/organism="Oryza sativa"
/mol_type="mRNA"
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/dev_stage="14 days after germination"
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/clone_lib="AtJMT-overexpressing transgenic rice lambda
phage cDNA library (JMT1)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      0.3%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1443 GCGCAGGC 1451
||| ||| |||
Db 1 GCACGAGGC 9

RESULT 78
CF325534/C
LOCUS
DEFINITION
JMT1--03-H24.g1 AtJMT-overexpressing transgenic rice lambda phage
cDNA library (JMT1) Oryza sativa cDNA clone JMT1--03-H24, mRNA
sequence.
ACCESSION
CF325534
VERSION
CF325534.1 GI:33799350
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 9)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1. .9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/clone_lib="AtJMT-overexpressing transgenic rice lambda
phage cDNA library (JMT1)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      0.3%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1443 GCGCAGGC 1451
||| ||| |||
Db 1 GCACGAGGC 9

RESULT 80
CF325552/c
LOCUS
DEFINITION
JMT1--03-N02.g1 AtJMT-overexpressing transgenic rice lambda phage
cDNA library (JMT1) Oryza sativa cDNA clone JMT1--03-N02, mRNA
sequence.
ACCESSION
CF325552
VERSION
CF325552.1 GI:33799583
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.

```

```

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
         Song,S.I., Kim,J.K., Kim,I.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
         Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
         of Bioscience and Bioinformatics, Myongji University
         Yongin, Kyeonggi, Korea
         Tel: 82 31 330 6193
         Fax: 82 31 321 6355
         Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="JMT1--03-N02"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="AtJMT-overexpressing transgenic rice lambda
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/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
         XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
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         methyltransferase overexpression line."

Query Match 0.3%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1;e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1877 GCTCATGC 1885
Db 9 GCTCGTGC 1

RESULT 81
BG925375 10 bp mRNA linear EST 06-NOV-2001
LOCUS HNC5-1-A9.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
DEFINITION sequence.
ACCESSION BG925375
VERSION BG925375.1 GI:14319898
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
         Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
         Lark,M.W.
TITLE Identification and initial characterization of 5000 expressed
         sequenced tags (ESTs) each from adult human normal and
         osteoarthritic cartilage cDNA libraries
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE 21482651
PUBMED 11597177
COMMENT Contact: Sanjay Kumar
         UW2109
         GlaxoSmithKline
         709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
         Tel: 610-270-7245
         Fax: 610-270-5598
         Email: sanjay.kumar-legsk.com
         Seq primer: T7.
         Location/Qualifiers
         1..10
         /organism="Homo sapiens"
         /mol_type="mRNA"

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
         Song,S.I., Kim,J.K., Kim,I.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
         Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
         of Bioscience and Bioinformatics, Myongji University
         Yongin, Kyeonggi, Korea
         Tel: 82 31 330 6193
         Fax: 82 31 321 6355
         Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa"
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/lab_host="E.coli SOLR"
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/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
         XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
         end with EcoRI and 3' end with XhoI site. mRNA was
         prepared from Arabidopsis jasmonate Carboxyl
         methyltransferase overexpression line."

Query Match 0.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1240 CTCGCCTCC 1248
Db 1 CTCGCATCC 9

RESULT 82
BM396082 10 bp mRNA linear EST 17-JAN-2002
LOCUS 5009-0-16-H04.t.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM396082
VERSION BM396082.1 GI:18196135
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 10)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
         Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
COMMENT Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..10
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript 2 SK+; Details on library
         preparation can be found in Chilcoat and Turkewitz (2001)
         Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1334 ACCCGCTGG 1342
Db 2 ACCGCGTGG 10

RESULT 83
BM396082/c 10 bp mRNA linear EST 17-JAN-2002
LOCUS 5009-0-16-H04.t.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM396082
VERSION BM396082.1 GI:18196135
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.

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Query Match	0.3%;	Score 7.4;	DB 1;	Length 10;
Best Local Similarity	88.9%;	Pred. No. 22;		
Matches	8;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0;
QY	1206	CTATCAGGG 1214		
DB				
	9	CTATCAGAG 1		
RESULT 85				
CF311011				
LOCUS		10 bp	mRNA	linear EST 15-AUG-2003
DEFINITION	ABF--06-B02.b1 ABF3-overexpressing transgenic rice plasmid cDNA			
ACCESSION	library (ABF) Oryza sativa cDNA clone ABF--06-B02, mRNA sequence.			
VERSION	CF311011			
KEYWORDS	EST.			
SOURCE	CF311011.1 GI:33682772			
ORGANISM	Oryza sativa			
	Oryza sativa			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Ehrhartoideae; Magnoliophyta; Liliopsida; Poales; Poaceae;			
	1 (bases 1 to 10)			
REFERENCE	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,			
AUTHORS	Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.			
TITLE	Large-scale Sequencing Analysis of Rice ESTs			
JOURNAL	Contact: Nahm B.H.			
COMMENT	Unpublished (2003)			
	Genomics and Genetics Institute, GreenGene Biotech Inc.; Division			
	of Bioscience and Bioinformatics, Myongji University			
	Yongin, Kyeonggi, Korea			
	Tel: 82 31 330 6193			
	Fax: 82 31 321 6355			
	Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.			
FEATURES	Location/Qualifiers			
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	/tissue_type="leaf"			
	/dev_stage="14 days after germination"			
	/lab_host="E.coli DH10B"			
	/clone_lib="ABF3-overexpressing transgenic rice plasmid			
	cDNA library (ABF)"			
	/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried			
	for 2hrs. Oligo-capped mRNA was reverse transcribed and			
	then used for PCR. mRNA was prepared from ABA-responsive			
	element binding transcription factor 3 overexpression			
	line."			
Query Match	0.3%;	Score 7.4;	DB 1;	Length 10;
Best Local Similarity	88.9%;	Pred. No. 22;		
Matches	8;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0;
QY	934	CTCCTCTTC 942		
DB				
	2	CTCCTCTTC 10		
RESULT 86				
CF311011/c				
LOCUS		10 bp	mRNA	linear EST 15-AUG-2003
DEFINITION	ABF--06-B02.b1 ABF3-overexpressing transgenic rice plasmid cDNA			
ACCESSION	library (ABF) Oryza sativa cDNA clone ABF--06-B02, mRNA sequence.			
VERSION	CF311011			
KEYWORDS	EST.			
SOURCE	CF311011.1 GI:33682772			
ORGANISM	Oryza sativa			
	Oryza sativa			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			

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Seq primer: T3.
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/organism="Theobroma cacao"
/mol_type="mRNA"
source

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RESULT	89
LOCUS	BH169696/c
DEFINITION	BH169696 12 bp DNA linear GSS 03-OCT-2001 SALK_001766 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_001766, genomic survey sequence.
ACCESSION	BH169696
VERSION	BH169696.1 GI:15905071

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KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
AUTHORS 1 (bases 1 to 12)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,I.,
Shinn,P., Zimmermann,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Saik Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 553 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1. .12
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
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/clone.lib="Arabidopsis thaliana TDNA insertion lines"
/clone.pcr="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
Query Match 0.3%; Score 7.4; DB 1; Length 12;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1577 TTGGGGCC 1585
Db 10 TTGGGGCC 2
RESULT 90
BQ591624 12 bp mRNA linear EST 06-DEC-2002
LOCUS BQ591624
DEFINITION CDNA clone 024-017-P07-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
ACCESSION BQ591624
VERSION BQ591624.1 GI:26121207
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
AUTHORS 1 (bases 1 to 12)
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL MEDLINE 22362189
PUBMED 12472698
Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
GSS.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 12)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,I.,
Shinn,P., Zimmermann,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Saik Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 553 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1. .12
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
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/clone.pcr="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
Query Match 0.3%; Score 7.4; DB 1; Length 12;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1577 TTGGGGCC 1585
Db 10 TTGGGGCC 2
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BQ591624 12 bp mRNA linear EST 06-DEC-2002
LOCUS BQ591624
DEFINITION CDNA clone 024-017-P07-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
ACCESSION BQ591624
VERSION BQ591624.1 GI:26121207
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
AUTHORS 1 (bases 1 to 12)
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL MEDLINE 22362189
PUBMED 12472698
Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissnaempiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 17 row: P column: 07
Seq primer: SP6; CATACGATTAGTGACACTATAG.
FEATURES
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line)"
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/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCAGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
Query Match 0.3%; Score 7.4; DB 1; Length 12;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 996 TTGTGGGAA 1004
Db 1 TTTTGGGAA 9
RESULT 91
CF339091 8 bp mRNA linear EST 18-AUG-2003
LOCUS CF339091
DEFINITION RCL1--03-M05.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa cDNA clone RCL1--03-M05, mRNA sequence.
ACCESSION CF339091
VERSION CF339091.1 GI:33826564
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS 1 (bases 1 to 8)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of BioScience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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(RC11)"
 /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
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 regenerated media"

Query Match 0.3%; Score 7; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1141 AGCTCCA 1147
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 Db 8 AGCTCCA 2

RESULT 92
 CF295648
 LOCUS
 DEFINITION 8 bp mRNA linear EST 14-AUG-2003
 sativa cDNA clone 30DGS--05-K23, mRNA sequence.

CF295648
 CF295648 1 GI:33664681
 EST.

ORYZA SATIVA
 Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 8)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
 source

1. .8
 Location/Qualifiers
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="30DGS--05-K23"
 /tissue_type="leaf"
 /dev_stage="30 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.3%; Score 7; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 ATATACC 325
 |||||
 Db 2 ATATACC 8

RESULT 93
 CF921494
 LOCUS
 DEFINITION 8 bp mRNA linear EST 05-NOV-2003
 gmhrRw3-10 B07_1_061 Soybean root hair subtracted cDNA library

CF921494
 CF921494 1 GI:38192288
 EST.

SOURCE
 ORGANISM

Glycine max (soybean)
 Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.

REFERENCE 1 (bases 1 to 8)

AUTHORS Scheffler, B.E., Huang, S., Liu, X., Nguyen, H., Duke, M. and Stacey, G.
 TITLE Expressed sequence tags from soybean root hair subtractive cDNA
 library

JOURNAL Unpublished (2003)

COMMENT Contact: Gary Stacey
 University of Missouri
 108 Waters Hall, Columbia, MO 65211, USA
 Tel: 573-884-4752

Fax: 573-884-0588
 Email: stacey@missouri.edu

Single pass sequence
 Seq primer: T7

FEATURES
 source

1. .8
 Location/Qualifiers
 /organism="Glycine max"
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 /cultivar="Williams 82"
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 /clone_lib="Soybean root hair subtracted cDNA library
 gmhrRw3"

/note="Organ: root hairs; Vector: pCR2-1 Topo; cDNA clones
 generated from soybean root hair tissue treated with
 Bradyrhizobium japonicum for 3 hours."

Query Match 0.3%; Score 7; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1973 TGTGTTT 1979
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 Db 2 TGTGTTT 8

RESULT 94
 CA851350/c

LOCUS
 DEFINITION 8 bp mRNA linear EST 01-AUG-2003
 D12G08 N20 14.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max

cDNA clone D12G08 5', mRNA sequence.

CA851350

CA851350 1 GI:33388143

EST.

KEYWORDS Glycine max (soybean)

SOURCE

Glycine max
 Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.

REFERENCE 1 (bases 1 to 8)

AUTHORS Alkharouf, N.W., Khan, R. and Matthews, B.F.

TITLE Analysis of expressed sequence tags from roots of resistant soybean
 infected by the soybean cyst nematode

JOURNAL Unpublished (2002)

COMMENT Contact: Alkharouf, N.W.

Soybean Genomics and Improvement Laboratory (SGIIL)

US Department of Agriculture (USDA), ARS, PSI
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 USA

Tel: 301 504 5750

Fax: 301 504 5728

Email: alkharouf@ars.usda.gov.

FEATURES
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1. .8
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Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1889 TTTTGGGT 1896
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Db 8 TTTTGGGT 1

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library (HD) Oryza sativa cDNA clone HD--01-P12, mRNA sequence.
ACCESSION CF313731
VERSION CF313731.1 GI:33685492
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 8)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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      line."

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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
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Db 8 AAAACCA 2

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extracted from Peking roots 2 and 4 days past invasion."

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Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1889 TTTTGGGT 1896
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Db 8 TTTTGGGT 1

RESULT 95
CF313731/c
LOCUS
DEFINITION HD--01-P12.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--01-P12, mRNA sequence.
ACCESSION CF313731
VERSION CF313731.1 GI:33685492
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 8)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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      line."

Query Match      0.3%; Score 7; DB 1; Length 9;
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Db 7 CTTTGT 1

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Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM396043
VERSION BM396043.1 GI:18196096
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 10)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: r3.
Location/Qualifiers
      1..10
      /organism="Tetrahymena thermophila"

cDNA clone D16C10 5', mRNA sequence.
CA851674 GI:33388467
EST.
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 9)
Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
Location/Qualifiers
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      extracted from Peking roots 2 and 4 days past invasion."

Query Match      0.3%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2132 CTTTGT 2138
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Db 7 CTTTGT 1

RESULT 97
EM396043
LOCUS
DEFINITION 5009-0-15-H12.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM396043
VERSION BM396043.1 GI:18196096
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 10)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: r3.
Location/Qualifiers
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/notes="vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match          0.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 477 CCCGGG 483
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RESULT 98
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LOCUS          10 bp mRNA linear EST 17-JAN-2002
DEFINITION    5009-0-15-H12.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION    BM396043.1 GI:18196096
VERSION      EST.
SOURCE       Tetrahymena thermophila
ORGANISM     Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Frankel,J., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
CONTACT: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
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Location/Qualifiers
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preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1154 CCCCGG 1160
Db 9 CCCCGG 3

RESULT 99
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LOCUS          10 bp mRNA linear EST 18-AUG-2003
DEFINITION    HDN--05-A22.g1 OsHDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa cDNA clone HDN--05-A22, mRNA
sequence.
ACCESSION    CF323895.1 GI:33796055
VERSION      EST.
SOURCE       Oryza sativa
ORGANISM     Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 10)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 10)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
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derived from rice Histone Deacetylase overexpression
line."

Query Match          0.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 GCCCGAG 123
Db 1 GCCCGAG 7

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DEFINITION    HDN--05-A22.g1 OsHDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa cDNA clone HDN--05-A22, mRNA
sequence.
ACCESSION    CF323895
VERSION      CF323895.1 GI:33796055
KEYWORDS     EST.
SOURCE       Oryza sativa
ORGANISM     Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 10)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.3%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 37;
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 Db 10 GCCCTCG 4

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 VERSION CF336905.1 GI:33822181
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1. (bases 1 to 10)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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QY 1017 AAAAGAG 1023
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 Db 1 AAAAGAG 7

RESULT 102
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LOCUS
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 KEYWORDS EST.
 SOURCE Tetrahymena thermophila
 ORGANISM Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymena.
 1. (bases 1 to 11)
 Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,
 Frankel, J. and Klobutcher, L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.

FEATURES
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 preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.3%; Score 7; DB 1; Length 11;
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RESULT 103
 BG927412/C
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 sequence.
 ACCESSION BG927412
 VERSION BG927412.1 GI:14321935
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1. (bases 1 to 11)
 Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,
 Satche, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and
 Lark, M.W.
 Identification and initial characterization of 5000 expressed
 sequenced tags (ESTs) each from adult human normal and
 osteoarthritic cartilage cDNA libraries
 Osteoarthr. Cartil. 9 (7), 641-653 (2001)

Query Match 0.3%; Score 7; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1352 TGCCCCC 1358
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 Db 3 TGCCCCC 9

RESULT 103
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 LOCUS
 DEFINITION HNC1-1-G11.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
 sequence.
 ACCESSION BG927412
 VERSION BG927412.1 GI:14321935
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1. (bases 1 to 11)
 Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,
 Satche, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and
 Lark, M.W.
 Identification and initial characterization of 5000 expressed
 sequenced tags (ESTs) each from adult human normal and
 osteoarthritic cartilage cDNA libraries
 Osteoarthr. Cartil. 9 (7), 641-653 (2001)

Query Match 0.3%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 37;
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QY 1017 AAAAGAG 1023
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 Db 1 AAAAGAG 7

CONTACT: Sanjay Kumar
 GlaxoSmithKline
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
 Tel: 610-270-7245
 Fax: 610-270-5598

RESULT 105

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

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Location/Qualifiers
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Db 9 GTCAGGT 3

RESULT 107
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LOCUS
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ACCESSION BG925375
VERSION BG925375.1 GI:14319898
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J., Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and Lark, M.W.
TITLE Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE 21482651
PUBMED 11597177
COMMENT Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@gsk.com

FEATURES

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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI; Directional"

Query Match 0.3%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 77 AGGAGGGGAG 86
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Db 10 AGGATCGGAG 1

RESULT 108
CF333615/c
LOCUS
DEFINITION JMT--02-J09.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--02-J09, mRNA sequence.
ACCESSION CF333615
VERSION CF333615.1 GI:33815525
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 10)

REFERENCE
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES source

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Location/Qualifiers
/organism="Oryza sativa"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--02-J09"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.3%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 380 GTGTGTGTCC 389

Db 10 GTCAGTGTCC 1

RESULT 109
CF336905/c
LOCUS
DEFINITION JMT--07-C04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--07-C04, mRNA sequence.
ACCESSION CF336905
VERSION CF336905.1 GI:33822181
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 10)
REFERENCE
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

```

TITLE
JOURNAL
COMMENT
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/tissue type="leaf"
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/lab host="E.coli DH10B"
/clone lib="ATJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.3%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 594 GATCTCTTCT 603
Db 10 GAACCTCTTTT 1

RESULT 110
BQ590709 11 bp mRNA linear EST 06-DEC-2002
DEFINITION E012597-024-018-024-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
cDNA clone 024-018-024 5-PRIME, mRNA sequence.
ACCESSION BQ590709
VERSION BQ590709.1 GI:26120292
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 11)
Herwig,R.; Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Email: weisshaar@mpiz-koeln.mpg.de
Fax: 00492215062851
Insert Length: 11 Std Error: 0.00
Plate: 18 row: 0 column: 24
Seq primer: SP6; CATACGATTAGTGACACTATAG.
Location/Qualifiers
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/organism="Beta vulgaris"
/mol type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:189410"

TITLE
JOURNAL
COMMENT
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..11
/organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDN-01-M19"
/tissue type="callus"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/lab host="E.coli SOLR"
/clone lib="OSHAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 6.8; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 72;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1301 AGAGCTTAGA 1310
Db 1 AGAGCTTTGA 10

RESULT 111
CF322692 11 bp mRNA linear EST 18-AUG-2003
DEFINITION HDN--01-M19-g1 OshDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa cDNA clone HDN--01-M19, mRNA
sequence.
ACCESSION CF322692
VERSION CF322692.1 GI:33793616
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..11
/organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDN-01-M19"
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/dev stage="proliferated callus on 2N6 media for 2 weeks"
/lab host="E.coli SOLR"
/clone lib="OSHAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 6.8; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 72;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1494 GCGGAGGCC 1503
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Db 1 GCACGAGGCC 10

RESULT 112
LOCUS AQ050979
DEFINITION nbxb0004d11r CUGI Rice BAC Library Oryza sativa (japonica cultivar-group) genomic clone nbxb0004H22r, genomic survey sequence.
ACCESSION AQ050979
VERSION AQ050979.2 GI:4501770
KEYWORDS GSS.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
REFERENCE 1 (bases 1 to 12)
AUTHORS Wing, R.A. and Dean, R.A.
TITLE A BAC End Sequencing Framework to Sequence the Rice Genome
JOURNAL Unpublished (1998)
COMMENT On Mar 23, 1999 this sequence version replaced gi:3325284.
Contact: Wing RA
Clemson University
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 1.
FEATURES
    source
    location/Qualifiers
    1..12
        /organism="Oryza sativa (japonica cultivar-group)"
        /mol_type="genomic DNA"
        /strain="Japonica"
        /cultivar="Nipponbare"
        /db_xref="taxon:3994"
        /clone="nbxb0004H22r"
        /tissue_type="Leaf"
        /lab_host="E. coli DH10B"
        /clone_lib="CUGI Rice BAC Library"
        /note="Vector: pBelobAC11; Site 1: HindIII; Site 2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation of a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
Query Match 0.3%; Score 6.8; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 451 ACCTACTTGT 460
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Db 1 ACCTATTTT 10

RESULT 113
LOCUS BH170808
DEFINITION SALK_003378 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_003378, genomic survey sequence.
ACCESSION BH170808
VERSION BH170808.1 GI:15906490
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 13)
AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmermann, J. and Ecker, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.
FEATURES
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        /mol_type="genomic DNA"
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        /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
Query Match 0.3%; Score 6.8; DB 1; Length 13;
Best Local Similarity 80.0%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 288 GCCGCTGGTG 297
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Db 1 GCCGGCGGTG 10

RESULT 114
LOCUS CA798290/c
DEFINITION Cac BL_611 Cac BL (Bean and Leaf from Amelonardo type Cacao) Theobroma cacao cDNA clone Cac BL_611 5', mRNA sequence.
ACCESSION CA798290
VERSION CA798290.1 GI:26055376
KEYWORDS EST.
SOURCE Theobroma cacao (cacao)
ORGANISM Theobroma cacao
REFERENCE 1 (bases 1 to 14)
AUTHORS Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D., Retzel, E.R. and Jones, C.A.
TITLE Gene discovery and microarray analysis of cacao (Theobroma cacao

```


DEFINITION HDAL--02-L22-g1 OshDAC1-overexpressing transgenic rice lambda phage
cDNA library I (HDAL) Oryza sativa cDNA clone HDAL--02-L22, mRNA
sequence.
ACCESSION CF306116
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE 1 (bases 1 to 8)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/lab_host="E.coli SOLR"
/clone_lib="OshDAC1-overexpressing transgenic rice lambda
phage cDNA library I (HDAL)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 827 GCACGAG 834
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Db 1 GCACGAGG 8

RESULT 118
CF306116/c
LOCUS
DEFINITION HDAL--02-L22-g1 OshDAC1-overexpressing transgenic rice lambda phage
cDNA library I (HDAL) Oryza sativa cDNA clone HDAL--02-L22, mRNA
sequence.

ACCESSION CF306116
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE 1 (bases 1 to 8)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source
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Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/clone_lib="OshDAC1-overexpressing transgenic rice lambda
phage cDNA library I (HDAL)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1878 CCTCATGC 1885
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Db 8 CCTCGTGC 1

RESULT 119

CF306762

LOCUS

DEFINITION HDAL--04-M13-g1 OshDAC1-overexpressing transgenic rice lambda phage
cDNA library I (HDAL) Oryza sativa cDNA clone HDAL--04-M13, mRNA
sequence.

ACCESSION CF306762

VERSION CF306762.1

KEYWORDS GI:33678523

SOURCE EST.

ORGANISM Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE 1 (bases 1 to 8)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDAL--04-M13"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OshDAC1-overexpressing transgenic rice lambda
phage cDNA library I (HDAL)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

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Query Match      0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      827 GCACGAAG 834
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Db      1 GCACGAGG 8

RESULT 120
CF306762/c
LOCUS
DEFINITION HDAL--04-M13.g1 OshDACL1-overexpressing transgenic rice lambda phage
            cDNA library I (HDAL) Oryza sativa cDNA clone HDAL--04-M13, mRNA
            sequence.
ACCESSION CF306762
VERSION   CF306762.1 GI:33678523
KEYWORDS EST.
SOURCE   Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 8)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
        Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyonggi, Korea
          Tel: 82 31 321 6355
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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            /organism="Oryza sativa"
            /mol_type="mRNA"
            /cultiVar="Nackdong"
            /db_xref="taxon:4530"
            /clone="HDAL--04-M13"
            /tissue_type="callus"
            /dev_stage="proliferated callus on 2N6 media for 2 weeks"
            /lab_host="E.coli SOLR"
            /clone_lib="OshDACL1-overexpressing transgenic rice lambda
            phage cDNA library I (HDAL)"
            /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
            XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
            was inserted into lambda Uni-ZAP XR vector at 5' end with
            EcoRI and 3' end with XhoI site. mRNA was derived from
            rice Histone Deacetylase overexpression line."

Query Match      0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1878 CCTCATGC 1885
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Db      8 CCTCGTGC 1

RESULT 121
CF322514
LOCUS
DEFINITION HDN--01-E13.g1 OshDACL1-overexpressing transgenic rice lambda phage
            cDNA library II (HDN) Oryza sativa cDNA clone HDN--01-E13, mRNA
            sequence.
ACCESSION CF322514
VERSION   CF322514.1 GI:33793267
KEYWORDS EST.
SOURCE   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 8)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
        Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyonggi, Korea
          Tel: 82 31 321 6355
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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            /mol_type="mRNA"
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            /db_xref="taxon:4530"
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            /lab_host="E.coli SOLR"
            /clone_lib="OshDACL1-overexpressing transgenic rice lambda
            phage cDNA library I (HDAL)"
            /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
            XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
            was inserted into lambda Uni-ZAP XR vector at 5' end with
            EcoRI and 3' end with XhoI site. mRNA was derived from
            rice Histone Deacetylase overexpression line."

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ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 8)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
        Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyonggi, Korea
          Tel: 82 31 321 6355
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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            /clone_lib="OshDACL1-overexpressing transgenic rice lambda
            phage cDNA library II (HDN)"
            /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
            XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
            5' end with EcoRI and 3' end with XhoI site. mRNA was
            derived from rice Histone Deacetylase overexpression
            line."

Query Match      0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      827 GCACGAAG 834
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Db      1 GCACGAGG 8

RESULT 122
CF322514/c
LOCUS
DEFINITION HDN--01-E13.g1 OshDACL1-overexpressing transgenic rice lambda phage
            cDNA library II (HDN) Oryza sativa cDNA clone HDN--01-E13, mRNA
            sequence.
ACCESSION CF322514
VERSION   CF322514.1 GI:33793267
KEYWORDS EST.
SOURCE   Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 8)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
        Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyonggi, Korea
          Tel: 82 31 321 6355
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Oryza sativa
Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
i. (bases 1 to 8)
Song, S.-S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Kim, J.-K., Kim, Y.-K. and Nahn, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

JOURNAL

COMMENT

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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/clone_lib="OshDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/note="vector: pBluescript SK(+); Site.1: EcoRI; Site.2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."
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Query Match 0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 827 GCACGAAG B34

Db 1 GCACGAGG 8

RESULT 126

CF323889/c

LOCUS

DEFINITION

8 bp mRNA linear EST 18-AUG-2003
HDN--05-A16.g1 OshDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa cDNA clone HDN--05-A16, mRNA
sequence.

ACCESSION CF323889

VERSION CF323889.1 GI:33796043

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 8)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

Tel: 82 31 321 6193

Fax: 82 31 321 6355

Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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/clone_lib="OshDAC1-overexpressing transgenic rice lambda
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phage cDNA library II (HDN)"

/note="vector: pBluescript SK(+); Site.1: EcoRI; Site.2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1878 CCTCATGC 1885

Db 8 CCTCGTGC 1

RESULT 127

CF324406

LOCUS

8 bp mRNA linear EST 18-AUG-2003
HDN--06-H05.g1 OshDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa cDNA clone HDN--06-H05, mRNA
sequence.

ACCESSION CF324406

VERSION CF324406.1 GI:33797080

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 8)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

Tel: 82 31 321 6193

Fax: 82 31 321 6355

Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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/clone="HDN--06-H05"

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/lab_host="E.coli SOLR"

/clone_lib="OshDAC1-overexpressing transgenic rice lambda

phage cDNA library II (HDN)"

/note="vector: pBluescript SK(+); Site.1: EcoRI; Site.2:

XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at

5' end with EcoRI and 3' end with XhoI site. mRNA was

derived from rice Histone Deacetylase overexpression

line."

Query Match

0.3%; Score 6.4; DB 1; Length 8;

Best Local Similarity 87.5%; Pred. No. 1.3e+02;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 827 GCACGAAG 834

Db 1 GCACGAGG 8

RESULT 128

CF324406/c

LOCUS

8 bp mRNA linear EST 18-AUG-2003
HDN--06-H05.g1 OshDAC1-overexpressing transgenic rice lambda phage

cDNA library II (HDN) Oryza sativa cDNA clone HDN-06-H05, mRNA sequence.
 CF324406
 VERSION
 CF324406.1 GI:33797080
 KEYWORDS
 EST.
 SOURCE
 ORGANISM
 Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 8)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 6.4; DB 1; Length 8;
 Best Local Similarity 87.5%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1878 CCTCATGC 1885
 |||||
 Db 8 CCTCGTGC 1

RESULT 129
 CF325379
 LOCUS
 DEFINITION
 JMT1--03-B08-g1 AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1) Oryza sativa cDNA clone JMT1--03-B08, mRNA sequence.

ACCESSION
 VERSION
 CF325379.1 GI:33799039
 KEYWORDS
 EST.
 SOURCE
 ORGANISM
 Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
 AUTHORS
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193

FEATURES
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 /clone_lib="AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.3%; Score 6.4; DB 1; Length 8;
 Best Local Similarity 87.5%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 827 GCACGAGG 834
 |||||
 Db 1 GCACGAGG 8

RESULT 130
 CF325379/c
 LOCUS
 DEFINITION

CF325379
 JMT1--03-B08-g1 AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1) Oryza sativa cDNA clone JMT1--03-B08, mRNA sequence.
 ACCESSION
 VERSION
 CF325379.1 GI:33799039
 KEYWORDS
 EST.
 SOURCE
 ORGANISM
 Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
 AUTHORS
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

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Query Match      0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1878 CCTCATGC 1885
Db 8 CCTCGTGC 1

RESULT 131
CF325469
LOCUS      CF325469      8 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT1--03-F06.g1 AtJMT-overexpressing transgenic rice lambda phage
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            sequence.
ACCESSION  CF325469.1 GI:33799223
VERSION     CF325469
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 8)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

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            /mol_type="mRNA"
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            XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
            end with EcoRI and 3' end with XhoI site. mRNA was
            prepared from Arabidopsis Jasmonate Carboxyl
            methyltransferase overexpression line."

Query Match      0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1878 CCTCATGC 1885
Db 8 CCTCGTGC 1

RESULT 133
CF325485
LOCUS      CF325485      8 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT1--03-F22.g1 AtJMT-overexpressing transgenic rice lambda phage
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            sequence.
ACCESSION  CF325485
VERSION     CF325485.1 GI:33799255
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 8)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

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            /cultivar="Nackdong"

Query Match      0.3%; Score 6.4; DB 1; Length 8;
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Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 827 GCACGAG 834
Db 1 GCACGAG 8

RESULT 132
CF325469/c
LOCUS      CF325469/c    8 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT1--03-F06.g1 AtJMT-overexpressing transgenic rice lambda phage
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            sequence.
ACCESSION  CF325469.1 GI:33799223
VERSION     CF325469
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 8)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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            /clone="JMT1--03-F06"
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            prepared from Arabidopsis Jasmonate Carboxyl
            methyltransferase overexpression line."

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phage cDNA library (JMT1)"
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XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

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Query Match      0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 827 GCACGAG 834
DB 1 GCACGAG 8

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RESULT 134
CF325485/c
LOCUS
DEFINITION
Oryza sativa CDNA clone JMT1--03-F22, mRNA
sequence.
ACCESSION
CF325485
VERSION
CF325485.1 GI:33799255
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Oryza.
REFERENCE
1 (bases 1 to 8)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhah@gbio.com, bnhah@bio.myongji.ac.kr.
Location/Qualifiers
1..8

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    /dev_stage="14 days after germination"
    /lab_host="E.coli SOLR"
    /clone_lib="AtUMT-overexpressing transgenic rice lambda
    phage cDNA library (JMT1)"
    /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
    XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
    end with EcoRI and 3' end with XhoI site. mRNA was
    prepared from Arabidopsis Jasmonate Carboxyl
    methyltransferase overexpression line."

```

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Query Match      0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1878 CCTCATGC 1885
DB 8 CCTCATGC 1

```

```

RESULT 135
CF338362/c
LOCUS
DEFINITION
Oryza sativa CDNA clone RCL1--01-H06, mRNA sequence.
ACCESSION
CF338362
VERSION
CF338362.1 GI:33825117
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Oryza.
REFERENCE
1 (bases 1 to 8)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhah@gbio.com, bnhah@bio.myongji.ac.kr.
Location/Qualifiers
1..8

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```

FEATURES
source
    /organism="Oryza sativa"
    /mol_type="mRNA"
    /cultiivar="Nackdong"
    /db_xref="taxon:4530"
    /clone="RCL1--01-H06"
    /tissue_type="callus"
    /dev_stage="proliferated callus on 2N6 media for 30 days"
    /lab_host="E.coli SOLR"
    /clone_lib="Regenerated callus lambda phage cDNA library
    (RCL1)"
    /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
    XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
    end with SstI and 3' end with XhoI site. Callus was
    induced on 2N6 media for 30 days and cultured for 36hrs on
    regenerated media"

```

```

Query Match      0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1169 CCAACTTT 1176
DB 8 CCAGCTTT 1

```

```

RESULT 136
CF339016/c
LOCUS
DEFINITION
Oryza sativa CDNA clone RCL1--03-111, mRNA sequence.
ACCESSION
CF339016
VERSION
CF339016.1 GI:33826415
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Oryza.
REFERENCE
1 (bases 1 to 8)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

```

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FEATURES
source
    /organism="Oryza sativa"
    /mol_type="mRNA"
    /cultiivar="Nackdong"
    /db_xref="taxon:4530"
    /clone="JMT1--03-F22"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli SOLR"
    /clone_lib="AtUMT-overexpressing transgenic rice lambda
    phage cDNA library (JMT1)"
    /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
    XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
    end with EcoRI and 3' end with XhoI site. mRNA was
    prepared from Arabidopsis Jasmonate Carboxyl
    methyltransferase overexpression line."

```

```

Query Match      0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1878 CCTCATGC 1885
DB 8 CCTCATGC 1

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. .8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="RCL1--03-111"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match 0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1169 CCAACTTT 1176
|||||
Db 8 CCAGCTTT 1

RESULT 137

CF339699/c

LOCUS

DEFINITION RCL1--05-K22.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa cDNA clone RCL1--05-K22, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

TITLE

JOURNAL

COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. .8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="RCL1--05-K22"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was

induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match 0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1169 CCAACTTT 1176
|||||
Db 8 CCAGCTTT 1

RESULT 138

CF340204/c

LOCUS

DEFINITION RCL1--07-E15.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa cDNA clone RCL1--07-E15, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

TITLE

JOURNAL

COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. .8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="RCL1--07-E15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match 0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1169 CCAACTTT 1176
|||||
Db 8 CCAGCTTT 1

RESULT 139

CF921494/c

LOCUS

DEFINITION GmIRW3-10_B07_1_061 Soybean root hair subtracted cDNA library
GmIRW3 Glycine max cDNA, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

CF921494 8 bp mRNA linear EST 05-NOV-2003
Glycine max (soybean)

ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 8)
 Schaffner, B.E., Huang, S., Liu, X., Nguyen, H., Duke, M. and Stacey, G.
 Expressed sequence tags from soybean root hair subtractive cDNA
 library
 Unpublished (2003)
 CONTACT: Gary Stacey
 University of Missouri
 108 Waters Hall, Columbia, MO 65211, USA
 Tel: 573-884-4752
 Fax: 573-882-0588
 Email: stacey@missouri.edu
 Single pass sequence
 Seq primer: T7
 Location/Qualifiers
 1..8
 /organism="Glycine max"
 /mol_type="mRNA"
 /cultivar="Williams 82"
 /db_xref="taxon:3847"
 /issue_type="root hairs"
 /clone_lib="Soybean root hair subtracted cDNA library
 gmrHw3"
 /notes="Organ: root hairs; Vector: pCR2-1 Topo; cDNA clones
 generated from soybean root hair tissue treated with
 Bradyrhizobium japonicum for 3 hours."

Query Match 0.3%; Score 6.4; DB 1; Length 8;
 Best Local Similarity 87.5%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 734 AGAAACAG 741
 | |||||
 Db 8 AAAACAG 1

RESULT 140
 CA794554
 LOCUS
 DEFINITION
 Cac BL_1496 Cac BL (Bean and Leaf from Amelonardo type Cacao)
 Theobroma cacao cDNA clone Cac_BL_1496 5', mRNA sequence.
 ACCESSION
 CA794554
 VERSION
 CA794554.1 GI:26051630
 EST.
 SOURCE
 Theobroma cacao (cacao)
 ORGANISM
 Theobroma cacao
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
 Theobroma.

REFERENCE
 1 (bases 1 to 8)
 Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,
 Retzel, E.R. and Jones, C.A.
 Gene discovery and microarray analysis of cacao (Theobroma cacao
 L.) varieties
 Planta 216 (2), 255-264 (2002)
 JOURNAL
 MEDLINE
 PUBMED
 12447539
 COMMENT
 Contact: Jones, Paul
 Masterfoods
 3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
 Tel: +44 1664 416644
 Email: Paul.Jones@eu.affem.com
 Seq primer: T3
 Location/Qualifiers
 1..8
 /organism="Theobroma cacao"
 /mol_type="mRNA"
 /strain="Amelonado type"

FEATURES
 source
 1..8
 /organism="Theobroma cacao"
 /mol_type="mRNA"
 /strain="Amelonado type"

/db_xref="taxon:3641"
 /clone="Cac BL_1496"
 /tissue_type="Mature leaf and mature bean"
 /cell_type="Whole organ"
 /dev_stage="maturity"
 /lab_host="XL-1 Blue MRF"
 /clone_lib="Cac BL (Bean and Leaf from Amelonardo type
 Cacao)"
 /notes="Vector: pBK-CMV; Bean and leaf tissue from an
 Amelonado type Cacao tree."

Query Match 0.3%; Score 6.4; DB 1; Length 8;
 Best Local Similarity 87.5%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 222 CAAATGGG 229
 | |||||
 Db 1 CAAAAGGG 8

RESULT 141
 CA794554/c
 LOCUS
 DEFINITION
 Cac BL_1496 Cac BL (Bean and Leaf from Amelonardo type Cacao)
 Theobroma cacao cDNA clone Cac_BL_1496 5', mRNA sequence.
 ACCESSION
 CA794554
 VERSION
 CA794554.1 GI:26051630
 EST.
 SOURCE
 Theobroma cacao (cacao)
 ORGANISM
 Theobroma cacao
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
 Theobroma.

REFERENCE
 1 (bases 1 to 8)
 Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,
 Retzel, E.R. and Jones, C.A.
 Gene discovery and microarray analysis of cacao (Theobroma cacao
 L.) varieties
 Planta 216 (2), 255-264 (2002)
 JOURNAL
 MEDLINE
 PUBMED
 12447539
 COMMENT
 Contact: Jones, Paul
 Masterfoods
 3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
 Tel: +44 1664 416644
 Email: Paul.Jones@eu.affem.com
 Seq primer: T3
 Location/Qualifiers
 1..8
 /organism="Theobroma cacao"
 /mol_type="mRNA"
 /strain="Amelonado type"
 /db_xref="taxon:3641"
 /clone="Cac BL_1496"
 /tissue_type="Mature leaf and mature bean"
 /dev_stage="maturity"
 /lab_host="XL-1 Blue MRF"
 /clone_lib="Cac BL (Bean and Leaf from Amelonardo type
 Cacao)"
 /note="Vector: pBK-CMV; Bean and leaf tissue from an
 Amelonado type Cacao tree."

Query Match 0.3%; Score 6.4; DB 1; Length 8;
 Best Local Similarity 87.5%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1886 CCGTTTTC 1893
 | |||||
 Db 8 CCGTTTC 1

RESULT 142
 CA794554/c
 LOCUS
 DEFINITION
 Cac BL_1496 Cac BL (Bean and Leaf from Amelonardo type Cacao)
 Theobroma cacao cDNA clone Cac_BL_1496 5', mRNA sequence.
 ACCESSION
 CA794554
 VERSION
 CA794554.1 GI:26051630
 EST.
 SOURCE
 Theobroma cacao (cacao)
 ORGANISM
 Theobroma cacao
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
 Theobroma.

REFERENCE
 1 (bases 1 to 8)
 Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,
 Retzel, E.R. and Jones, C.A.
 Gene discovery and microarray analysis of cacao (Theobroma cacao
 L.) varieties
 Planta 216 (2), 255-264 (2002)
 JOURNAL
 MEDLINE
 PUBMED
 12447539
 COMMENT
 Contact: Jones, Paul
 Masterfoods
 3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
 Tel: +44 1664 416644
 Email: Paul.Jones@eu.affem.com
 Seq primer: T3
 Location/Qualifiers
 1..8
 /organism="Theobroma cacao"
 /mol_type="mRNA"
 /strain="Amelonado type"

FEATURES
 source
 1..8
 /organism="Theobroma cacao"
 /mol_type="mRNA"
 /strain="Amelonado type"

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RESULT 142
CA850813/c
LOCUS
DEFINITION
D06G10_G10_14.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
cDNA clone D06G10 5', mRNA sequence.
EST.
CA850813
VERSION
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 9)
Alkharouf, N.W., Khan, R. and Matthews, B.P.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
Location/Qualifiers
1..9
/organism="Glycine max"
/mol_type="cDNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D06G10"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/notes="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."
Query Match 0.3%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1957 CATAAGCA 1964
|||||
9 CATAAACA 2

Db

RESULT 143
CF323490/c
LOCUS
DEFINITION
CF323490
HDN--03-P21.g1 OshDACL-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa cDNA clone HDN--03-P21, mRNA
sequence.
EST.
CF323490
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 9)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

CA850813
D06G10_G10_14.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
cDNA clone D06G10 5', mRNA sequence.
EST.
CA850813
VERSION
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 9)
Alkharouf, N.W., Khan, R. and Matthews, B.P.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
Location/Qualifiers
1..9
/organism="Glycine max"
/mol_type="cDNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D06G10"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/notes="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."
Query Match 0.3%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1957 CATAAGCA 1964
|||||
9 CATAAACA 2

Db

RESULT 144
CA794225/c
LOCUS
DEFINITION
CA794225
Cac BL 1208 Cac BL (Bean and Leaf from Amelonardo type Cacao)
Theobroma cacao cDNA clone Cac BL_1208 5', mRNA sequence.
EST.
CA794225
VERSION
KEYWORDS
SOURCE
ORGANISM
Theobroma cacao (cacao)
Theobroma cacao
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eucosids II; Malvales; Malvaceae; Byttnerioideae;
Theobroma.
1 (bases 1 to 9)
Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,
Retzel, E.R. and Jones, C.A.
Gene discovery and microarray analysis of cacao (Theobroma cacao
L.) varieties
Planta 216 (2), 255-264 (2002)
22337596
12447539
Contact: Jones, Paul
Masterfoods
3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
Tel: +44 1664 416644
Email: Paul.Jones@eu.effem.com
Seq primer: T3.
Location/Qualifiers
1..9
/organism="Theobroma cacao"
/mol_type="mRNA"
/strain="Amelonado type"
/db_xref="taxon:3641"
/clone="Cac BL 1208"
/tissue_type="Mature leaf and mature bean"
/cell_type="Whole organ"
/dev_stage="maturity"
/lab_host="XL-1 Blue MRF"
/clone_lib="Cac BL (Bean and Leaf from Amelonardo type
Cacao)"
/notes="Vector: pBK-CMV; Bean and leaf tissue from an
Amelonado type Cacao tree."

```

```

Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDN--03-P21"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDA1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match 0.3%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1878 CCTCATGC 1885
|||||
8 CCTCGTGC 1

Db

RESULT 144
CA794225/c
LOCUS
DEFINITION
CA794225
Cac BL 1208 Cac BL (Bean and Leaf from Amelonardo type Cacao)
Theobroma cacao cDNA clone Cac BL_1208 5', mRNA sequence.
EST.
CA794225
VERSION
KEYWORDS
SOURCE
ORGANISM
Theobroma cacao (cacao)
Theobroma cacao
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eucosids II; Malvales; Malvaceae; Byttnerioideae;
Theobroma.
1 (bases 1 to 9)
Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,
Retzel, E.R. and Jones, C.A.
Gene discovery and microarray analysis of cacao (Theobroma cacao
L.) varieties
Planta 216 (2), 255-264 (2002)
22337596
12447539
Contact: Jones, Paul
Masterfoods
3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
Tel: +44 1664 416644
Email: Paul.Jones@eu.effem.com
Seq primer: T3.
Location/Qualifiers
1..9
/organism="Theobroma cacao"
/mol_type="mRNA"
/strain="Amelonado type"
/db_xref="taxon:3641"
/clone="Cac BL 1208"
/tissue_type="Mature leaf and mature bean"
/cell_type="Whole organ"
/dev_stage="maturity"
/lab_host="XL-1 Blue MRF"
/clone_lib="Cac BL (Bean and Leaf from Amelonardo type
Cacao)"
/notes="Vector: pBK-CMV; Bean and leaf tissue from an
Amelonado type Cacao tree."

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Query Match      0.3%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 961 TACCAACG 968
   |||||
Db 8 TATCAACG 1

RESULT 145
LOCUS      CA850899
DEFINITION D07H02.014.15.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
ACCESSION  CA850899
VERSION     CA850899.1 GI:33387692
KEYWORDS   Glycine max (soybean)
SOURCE     Glycine max
ORGANISM   Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Rosids; Magnoliophyta; eudicotyledons; core eudicots;
Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE  1 (bases 1 to 9)
AUTHORS   Alkharouf, N.W., Khan, R. and Matthews, B.F.
TITLE     Analysis of expressed sequence tags from roots of resistant soybean
JOURNAL   Unpublished (2002)
COMMENT   Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
Location/Qualifiers
1..9
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D07H02"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

Query Match      0.3%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1222 CCCATCCT 1229
   |||||
Db 9 CCCATCAT 2

RESULT 147
LOCUS      CF307008
DEFINITION HDAL-05-H11.g1 OsHDAC1-overexpressing transgenic rice lambda phage
ACCESSION  CF307008
VERSION     CF307008.1 GI:33678769
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE  1 (bases 1 to 9)
AUTHORS   Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT   Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDAL-05-H11"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLr"
/clone_lib="OsHDAC1-overexpressing transgenic rice lambda
phage cDNA library I (HDAL)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:

Query Match      0.3%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1862 GATGAGGG 1869
   |||||
Db 1 GATGATGG 8

RESULT 146
LOCUS      CA850899/c
DEFINITION D07H02.014.15.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
ACCESSION  CA850899
VERSION     CA850899.1 GI:33387692
KEYWORDS   Glycine max (soybean)
SOURCE     Glycine max
ORGANISM   Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eudicots I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE  1 (bases 1 to 9)

```

```

AUTHORS   Alkharouf, N.W., Khan, R. and Matthews, B.F.
TITLE     Analysis of expressed sequence tags from roots of resistant soybean
JOURNAL   Unpublished (2002)
COMMENT   Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
Location/Qualifiers
1..9
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D07H02"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

Query Match      0.3%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1222 CCCATCCT 1229
   |||||
Db 9 CCCATCAT 2

RESULT 147
LOCUS      CF307008
DEFINITION HDAL-05-H11.g1 OsHDAC1-overexpressing transgenic rice lambda phage
ACCESSION  CF307008
VERSION     CF307008.1 GI:33678769
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE  1 (bases 1 to 9)
AUTHORS   Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT   Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDAL-05-H11"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLr"
/clone_lib="OsHDAC1-overexpressing transgenic rice lambda
phage cDNA library I (HDAL)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:

```

XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 827 GCACGAG 834

Db 1 GCACGAG 8

RESULT 148
CF307008/c

LOCUS HDAL-05-H11.g1 OshDAC1-overexpressing transgenic rice lambda phage CDNA library I (HDAL) Oryza sativa cDNA clone HDAL-05-H11, mRNA sequence.
DEFINITION

ACCESSION CF307008

VERSION CF307008.1

KEYWORDS GI:33678769

SOURCE EST.

ORGANISM Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 9)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Source

1..9

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="HDAL-05-H11"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli SOLR"

/clone_lib="OshDAC1-overexpressing transgenic rice lambda phage CDNA library I (HDAL)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 6.4; DB 1; Length 9;

Best Local Similarity 87.5%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1878 CCTCATGC 1885

Db 8 CCTCATGC 1

RESULT 149
CF307092/c

LOCUS HDAL-05-L14.g1 OshDAC1-overexpressing transgenic rice lambda phage CDNA library I (HDAL) Oryza sativa cDNA clone HDAL-05-L14, mRNA sequence.

ACCESSION

VERSION CF307092.1

KEYWORDS GI:33678853

SOURCE EST.

ORGANISM Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 9)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Source

1..9

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="HDAL-05-L14"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli SOLR"

/clone_lib="OshDAC1-overexpressing transgenic rice lambda phage CDNA library I (HDAL)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match

Best Local Similarity 0.3%; Score 6.4; DB 1; Length 9;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1026 GGAGCTTG 1033

Db 8 GGAGCTGC 1

RESULT 150

CF309109

LOCUS

DEFINITION

ABF-03-C20.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF-03-C20, mRNA sequence.

ACCESSION CF309109

VERSION CF309109.1

KEYWORDS GI:33680870

SOURCE EST.

ORGANISM Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 9)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

```

source
1. .9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="ABF-03-C20"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match
Best Local Similarity 0.3%; Score 6.4; DB 1; Length 9;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 769 TTCTTCT 776
Db 2 TTCTTCT 9

RESULT 151
CF323636
LOCUS
DEFINITION
HDN--04-F24.gi OSHDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa cDNA clone HDN--04-F24, mRNA
sequence.
ACCESSION
CF323636
VERSION
CF323636.1 GI:33795531
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 9)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDN--04-F24"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

FEATURES
source
1. .9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDN--04-F24"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match
Best Local Similarity 0.3%; Score 6.4; DB 1; Length 9;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 746 CCGTGTGC 753
Db 8 CCGTGTGC 1

RESULT 153
CF325619
LOCUS
DEFINITION
JMT1--03-L16.gi AtJMT-overexpressing transgenic rice lambda phage
cDNA library (JMT1) Oryza sativa cDNA clone JMT1--03-L16, mRNA
sequence.
ACCESSION
CF325619
VERSION
CF325619.1 GI:33799518
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.

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QY 442 CACAAGG 449
Db 2 CACAAGG 9

RESULT 152
CF323636/c
LOCUS
DEFINITION
HDN--04-F24.gi OSHDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa cDNA clone HDN--04-F24, mRNA
sequence.
ACCESSION
CF323636
VERSION
CF323636.1 GI:33795531
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 9)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDN--04-F24"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match
Best Local Similarity 0.3%; Score 6.4; DB 1; Length 9;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 746 CCGTGTGC 753
Db 8 CCGTGTGC 1

RESULT 153
CF325619
LOCUS
DEFINITION
JMT1--03-L16.gi AtJMT-overexpressing transgenic rice lambda phage
cDNA library (JMT1) Oryza sativa cDNA clone JMT1--03-L16, mRNA
sequence.
ACCESSION
CF325619
VERSION
CF325619.1 GI:33799518
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.

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```

end, mRNA sequence.
ACCESSION CK298980
VERSION CK298980.1 GI:39886896
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana

REFERENCE
1 (bases 1 to 10)
AUTHORS Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jil, H. and Baker, B.
TITLE Generation of EST sequences from Nicotiana benthamiana
JOURNAL Unpublished (2003)
COMMENT Other ESTs: EST761693
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: GTA ATA CGA CTC ACT ATA GGG C.
FEATURES
Location/Qualifiers
1..10
/morganism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NBM0J48"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-TonA"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."
Query Match 0.3%; Score 6.4; DB 1; Length 10;
Best Local Similarity 87.5%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 413 AAAATAAT 420
|||||
Db 8 AAAAAAAT 1

RESULT 157
BU238234/c
LOCUS BU238234
DEFINITION Descurainia sophia cDNA clone Ds01_01e11, mRNA sequence.
ACCESSION BU238234
VERSION BU238234.1 GI:22750059
KEYWORDS EST.
SOURCE Descurainia sophia
ORGANISM Descurainia sophia

REFERENCE
1 (bases 1 to 11)
AUTHORS Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, I.J.,
Hattori, J.I., Ouellet, T., Robert, L.S., Spott, D. and Tinker, N.A.
TITLE Expressed Sequence Tags from Cold-Stressed Descurainia sophia
Seedlings
JOURNAL Unpublished (2001)
COMMENT Contact: Singh, J.A.

```

```

Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
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0C6, Canada
Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@em.agr.ca.
Location/Qualifiers
1..11
/morganism="Descurainia sophia"
/mol_type="mRNA"
/db_xref="taxon:89411"
/clone="Ds01_01e11"
/tissue_type="leaf, stem"
/dev_stage="1-month seedlings - 1 cm tall - 8 leaf"
/clone_lib="Ds01_AAFRC_ECRC_cold_stressed_Flixweed_seedling"
gs"
/note="Vector: Bluescript SK-/XhoI-EcoRI; Site 1: Eco RI;
Site 2: Xho I; Plants were grown for 1 month at 200C/16
hrs light/day (average 8 leaves, 1 cm tall, weight
0.02g/plant). Then they were exposed to 20C, 12 hrs
light/day, for 1 week. Library prepared by C. Piche using
Stratagene kit."
Query Match 0.3%; Score 6.4; DB 1; Length 11;
Best Local Similarity 87.5%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 593 AGATCTCT 600
|||||
Db 8 AGTCTCT 1

RESULT 158
CF543031
LOCUS CF543031
DEFINITION S015532-024-030-P02-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
024-030-P02 5-PRIME, mRNA sequence.
ACCESSION CF543031
VERSION CF543031.1 GI:34891471
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE
1 (bases 1 to 11)
AUTHORS Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL 22362189
MEDLINE
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 11 Std Error: 0.00
Plate: 30 row: P column: 02
Seq primer: SP6.
Location/Qualifiers
1..11
/morganism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:936732"
/db_xref="taxon:161934"
/clone="024-030-P02"
FEATURES
source

```

/tissue type="leaf"
/lab_host="EMDH10B"
/clone_lib="WP1Z-ADIS-024-leaf"
/note="Vector: PCWSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Finbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.3%; Score 6.2; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 76 GAGGAGGGGAG 86
|||||
Db 1 GGGGGGGGGGG 11

RESULT 159
CF338362
LOCUS
DEFINITION
RCL1--01-H06.g1 Regenerated callus lambda phage cDNA library (RCL1)
ACCESSION
CF338362
VERSION
CF338362.1 GI:33825117
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 8)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="RCL1--01-H06"
/tissue type="callus"
/dev stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library
(RCL1)"
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

Query Match 0.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2068 AAGCTG 2073
|||||
Db 2 AAGCTG 7

RESULT 161
CF339699
LOCUS
DEFINITION
RCL1--05-K22.g1 Regenerated callus lambda phage cDNA library (RCL1)
ACCESSION
CF339699
VERSION
CF339699.1 GI:33827769
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 8)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="RCL1--01-H06"
/tissue type="callus"
/dev stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library
(RCL1)"
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

Query Match 0.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2068 AAGCTG 2073
|||||
Db 2 AAGCTG 7

RESULT 160
CF339016
LOCUS

DEFINITION
RCL1--03-I11.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa cDNA clone RCL1--03-I11, mRNA sequence.
ACCESSION
CF339016
VERSION
CF339016.1 GI:33826415
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="RCL1--03-I11"
/tissue type="callus"
/dev stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library
(RCL1)"
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

FEATURES
source

Query Match 0.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2068 AAGCTG 2073
|||||
Db 2 AAGCTG 7

RESULT 161
CF339699
LOCUS
DEFINITION
RCL1--05-K22.g1 Regenerated callus lambda phage cDNA library (RCL1)
ACCESSION
CF339699
VERSION
CF339699.1 GI:33827769
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers
1..8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="RC11--05-K22"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RC11)"
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"
Query Match 0.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2068 AAGCTG 2073

Db 2 AAGCTG 7

RESULT 162

CF340204
LOCUS
DEFINITION
Oryza sativa CDNA clone RC11--07-E15, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

1 (bases 1 to 8)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 8)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1..8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="RC11--07-E15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RC11)"
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was

FEATURES

Location/Qualifiers
1..8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="RC11--07-E15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RC11)"
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was

induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match 0.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2068 AAGCTG 2073

Db 2 AAGCTG 7

RESULT 163

CA850825
LOCUS
DEFINITION
Oryza sativa CDNA clone D06H10 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

1 (bases 1 to 8)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 8)
Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
Location/Qualifiers
1..8
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D06H10"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

Query Match 0.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1848 GGGTGG 1853

Db 1 GGGTGG 6

FEATURES

Location/Qualifiers
1..8
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D06H10"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

Query Match 0.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1848 GGGTGG 1853

Db 1 GGGTGG 6

RESULT 164

CA850825/c
LOCUS
DEFINITION
Oryza sativa CDNA clone D06H10 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

1 (bases 1 to 8)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 8)
Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
Location/Qualifiers
1..8
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D06H10"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

Query Match 0.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

1 (bases 1 to 8)

Alkharouf, N.W., Khan, R. and Matthews, B.F.

Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode

Unpublished (2002)

Contact: Alkharouf, N.W.

Soybean Genomics and Improvement Laboratory (SGIL)

US Department of Agriculture (USDA), ARS, PSI

Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,

USA

Tel: 301 504 5750

Fax: 301 504 5728

Email: alkharouf@ba.ars.usda.gov.

Location/Qualifiers

FEATURES

source

1..8

/organism="Glycine max"

/mol_type="mRNA"

/cultivar="Peking"

/db_xref="taxon:3847"

/clone="D06H10"

/tissue_type="Roots"

/dev_stage="Seedlings"

/clone_lib="cDNA Peking library 2, 4 day SCN3"

/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."

Query Match

Best Local Similarity 0.3%; Score 6; DB 1; Length 8;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

405 CCACC 410

Db

6 CCACC 1

RESULT 165

CAB81350

LOCUS

DEFINITION CAB81350 D12G08 N20.14.abl cDNA Peking library 2, 4 day SCN3 Glycine max cDNA clone D12G08 5', mRNA sequence.

ACCESSION CAB81350

VERSION CAB81350.1

KEYWORDS EST.

SOURCE Glycine max (soybean)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 8)

AUthors Alkharouf, N.W., Khan, R. and Matthews, B.F.

Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode

Unpublished (2002)

Contact: Alkharouf, N.W.

Soybean Genomics and Improvement Laboratory (SGIL)

US Department of Agriculture (USDA), ARS, PSI

Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,

USA

Tel: 301 504 5750

Fax: 301 504 5728

Email: alkharouf@ba.ars.usda.gov.

Location/Qualifiers

1..8

/organism="Glycine max"

/mol_type="mRNA"

/cultivar="Peking"

/db_xref="taxon:3847"

/clone="D12G08"

/tissue_type="Roots"

/dev_stage="Seedlings"

FEATURES

source

1..8

/organism="Glycine max"

/mol_type="mRNA"

/cultivar="Peking"

/db_xref="taxon:3847"

/clone="D12G08"

/tissue_type="Roots"

/dev_stage="Seedlings"

/clone_lib="cDNA Peking library 2, 4 day SCN3"

/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."

Query Match

Best Local Similarity 0.3%; Score 6; DB 1; Length 8;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1064 ACCCAA 1069

Db

1 ACCCAA 6

RESULT 166

CF297970

LOCUS

DEFINITION CF297970 8 bp mRNA linear EST 15-AUG-2003

7LEAF--01-C16.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa cDNA clone 7LEAF--01-C16, mRNA sequence.

ACCESSION CF297970

VERSION CF297970.1

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 8)

AUthors Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongui University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..8

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="7LEAF--01-C16"

/tissue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match

Best Local Similarity 0.3%; Score 6; DB 1; Length 8;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1233 GACAGC 1238

Db

3 GACAGC 8

RESULT 167

CF297970/c

LOCUS

DEFINITION CF297970 8 bp mRNA linear EST 15-AUG-2003

7LEAF--01-C16.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa cDNA clone 7LEAF--01-C16, mRNA sequence.

ACCESSION CF297970

VERSION CF297970.1

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 8)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1..8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF-01-C16"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 GCTGTC 251

Db 8 GCTGTC 3

RESULT 168

CF313731

LOCUS HD--01-P12.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--01-P12, mRNA sequence.

ACCESSION CF313731.1 GI:33685492

VERSION EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 8)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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CF330558

LOCUS

DEFINITION NACL--06-F04.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--06-F04, mRNA sequence.

ACCESSION CF330558.1 GI:33809354

VERSION EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 8)

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FEATURES

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RESULT 170

CF330558/c

LOCUS

DEFINITION NACL--06-F04.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--06-F04, mRNA sequence.

ACCESSION CF330558

VERSION

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KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Cryzeae; Oryza.
REFERENCE 1 (bases 1 to 8)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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